



# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number 168511

TO: Anish Gupta  
Location: rem/3A59/3C18  
Art Unit: 1654  
Friday, May 12, 2006  
Case Serial Number: 09/759584

From: Toby Port  
Location: Biotech-Chem Library  
REM-1A59  
Phone: (571)272-2523  
  
toby.port@uspto.gov

### Search Notes

Dear Examiner Gupta,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Toby Port  
Technical Information Specialist  
STIC Biotech/Chem Library  
(571)272-2523



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# STIC SEARCH RESULTS FEEDBACK FORM

## Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher or contact*:

Mary Hale, Information Branch Supervisor  
Remsen Bldg. 01 D86  
571-272-2507

## Voluntary Results Feedback Form

➤ I am an examiner in Workgroup:  Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature  
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop-off or send completed forms to STIC-Biotech-Chem Library, Remsen Bldg.



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STIC-Biotech/ChemLib

188511

M9

From: Gupta, Anish  
Sent: Wednesday, May 03, 2006 2:14 PM  
To: STIC-Biotech/ChemLib  
Subject: SEARCH REQUEST

Search Request:

Name: Anish Gupta  
Examiner #: 73121  
date: 5-3-06'  
Art Unit: 1654  
Phone # 2-965  
Serial Number 09/759584  
Location: 3A59  
Mailbox #: 3C18

STIC-Biotech/ChemLib  
May 3 2006  
Anish Gupta

Please search the nucleic acid encoding the protein of SEQ ID NO 49, SEQ ID NO 59 and SEQ ID NO 48.

thank you

anish gupta

\*\*\*\*\*

Searcher: \_\_\_\_\_  
Searcher Phone: \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date completed: \_\_\_\_\_  
Searcher Prep Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

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Type of Search  
NA# \_\_\_\_\_ AA# \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure #: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

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Vendors and cost where applicable  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIS: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (Specify): \_\_\_\_\_

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4	414	100.0	414	6	AR050153	AR050153	Sequence
5	414	100.0	414	6	AR130272	AR130272	Sequence 48
6	414	100.0	414	6	I23728	I23728	Sequence
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8	414	100.0	414	6	AR374914	AR374914	Sequence
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DEFINITION Sequence 37 from Patent WO9416076.  
ACCESSION A39549  
VERSION A39549.1 GI:2295842  
KEYWORDS  
SOURCE unidentified  
ORGANISM unclassified sequences.  
REFERENCE 1 (bases 1 to 414)  
AUTHORS Dubock,A.C., Powell,K.A. and Rees,S.B.  
TITLE ANTIMICROBIAL-PROTEIN-PRODUCING ENDOSYMBIOTIC MICROORGANISMS  
JOURNAL Patent: WO 9416076-A 37 21-JUL-1994;  
ZENECA LTD (GB)  
COMMENT Other publication AU 5820494 940815.  
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DEFINITION Sequence 19 from Patent WO9721814.  
ACCESSION A63404  
VERSION A63404.1 GI:3717176  
KEYWORDS  
SOURCE unidentified  
ORGANISM unclassified sequences.  
REFERENCE 1 (bases 1 to 414)  
AUTHORS Broekaert,W.F., De,S.G., Rees and Sarah,B.  
TITLE ANTI-FUNGAL PROTEINS  
JOURNAL Patent: WO 9721814-A 19 19-JUN-1997;  
ZENECA LTD (GB)  
COMMENT Other publication AU 1105397 19970703.  
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ACCESSION AR050153  
VERSION AR050153.1 GI:5972145  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 414)  
AUTHORS Broekaert,W.F., Cammue,B.P.A., Osborn,R.W., Rees,S.B.,  
Terras,F.R.G. and Vanderleyden,J.  
TITLE Biotidal proteins  
JOURNAL Patent: US 5824869-A 48 20-OCT-1998;  
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DEFINITION Sequence 48 from patent US 5538525.
ACCESSION  I23728
VERSION     I23728.1 GI:1603598
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 414)
AUTHORS     Broekaert,W.F., Cammue,B.P.A., Osborn,R.W., Rees,S.B.,
            Terras,F.R.G. and Vanderleyden,J.
TITLE       Biocidal proteins
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DEFINITION Sequence 48 from patent US 6187904.
ACCESSION  AR130272
VERSION     AR130272.1 GI:14118169
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 414)
AUTHORS     Broekaert,W.F., Cammue,B.P.A., Osborn,R.W., Rees,S.B.,
            Terras,F.R.G. and Vanderleyden,J.
TITLE       Biocidal proteins
JOURNAL     Patent: US 6187904-A 48 13-FEB-2001;
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RESULT 6
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DEFINITION Sequence 48 from patent US 5538525.
ACCESSION  I23728
VERSION     I23728.1 GI:1603598
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 414)
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TITLE       Biocidal proteins
JOURNAL     Patent: US 5538525-A 48 23-JUL-1996;
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LOCUS AR207337 414 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 19 from patent US 6372888.
ACCESSION AR207337
VERSION AR207337.1 GI:21506219
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS De Samblanx,G.Wivina., Broekaert,W.Frans. and Rees,S.Bronwen.
TITLE Antifungal proteins
JOURNAL Patent: US 6372888-A 19 16-APR-2002;
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RESULT 9
AR642703
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DEFINITION Sequence 19 from patent US 6864068.
ACCESSION AR642703
VERSION AR642703.1 GI:62779939
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REFERENCE
AUTHORS Rees,S.B., De Samblanx,G.W. and Broekaert,W.F.
TITLE Antifungal proteins
JOURNAL Patent: US 6864068-A 19 08-MAR-2005;
Syngenta Limited; Guilford;
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QY 301 ACAAAATAAGTCAGTGTCACTATCCATGAGTGATTTAAGACATGTACCAGATATGTTAT 360
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RESULT 8
AR374914
LOCUS AR374914 414 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 45 from patent US 6605698.
ACCESSION AR374914
VERSION AR374914.1 GI:40077932
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Van Amerongen,A., Pant,F., Borremans,F.A., De Samblanx,G.W., Sijtsma,L., Meeloen,R.H., Fuijk,W.C., Schaaper,W.M.M., Broekaert,W.F., van Gelder,W.M.J. and Rees,S.B.
TITLE Antifungal peptides and composition thereof
JOURNAL Patent: US 6605698-A 45 12-AUG-2003;
Syngenta Limited; Guilford;
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QY 121 CCAAGTGGGACATGGTCAGGAGTCTGTGGAACAATTAACGCATGCAAGATCAGTGCATT 180
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DB 361 GTTGGTTCGGTTATACAAATAAAGTTTATTCCACCAAAAAA 414
RESULT 9
AR642703
LOCUS AR642703 414 bp DNA linear PAT 20-APR-2005
DEFINITION Sequence 19 from patent US 6864068.
ACCESSION AR642703
VERSION AR642703.1 GI:62779939
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Rees,S.B., De Samblanx,G.W. and Broekaert,W.F.
TITLE Antifungal proteins
JOURNAL Patent: US 6864068-A 19 08-MAR-2005;
Syngenta Limited; Guilford;
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source
Location/Qualifiers
1. .414
/organism="unknown"
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ORIGIN
Query Match 100.0%; Score 414; DB 6; Length 414;
Best Local Similarity 100.0%; Pred. No. 1.4e-82;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTTATTAGTCATCGCTAAGTTTGGGTCCATCATCGCACTTCTTTTGGTCTCTT 60
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QY 61 GTTCTTTTGGTCTTTTGAAGCACCACCAATGGTGAAGCACAAGTTGTGCGAAAGG 120
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QY 121 CCAAGTGGGACATGGTCAGGAGTCTGTGGAACAATTAACGCATGCAAGATCAGTGCATT 180
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QY 181 AACCTTGAGAAAGCAGCAGCATGGATCTTGCACACTATGTCTTCCAGCTCACAAAGTGATC 240
DB 181 AACCTTGAGAAAGCAGCAGCATGGATCTTGCACACTATGTCTTCCAGCTCACAAAGTGATC 240
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QY 4 TTATTAGTCATCGCTAAGTTTGGTCCATCATCGCACTCTTTTGGCTGCTCTGTT 63
Db 29 TTAGTAGTCATCGCTAAGTTTGGTCCATCATCTTCTCTTCTGCTGCTCTGTC 88

QY 64 CTTTTTGTGCTTTTGAAGCACCACCAATAGTGTGGAAGCAGCAAGTTGTGCGAAGGCCA 123
Db 89 GTTTTCTGCTTTTGAAGCACCACCAATAGTGTGGAAGCAGCAAGTTGTGTCAGAGGCCA 148

QY 124 AGTGGACATGGTCAGGAGTCTGTGGAACAATAACGCAATGCAAGAAATCAGTGCATTAA 183
Db 149 AGTGGACATGGTCAGGAGTCTGTGGAATAATAACGCAATGCAAGAAATCAGTGCATTCA 208

QY 184 CTTGAGAAAGCAGCATCGATCTTGCACACTATGTCTTCCAGCTCACAAAGTGTATCTGC 243
Db 209 CTTGAGAAAGCAGCATCGATCTTGCACACTATGTCTTCCAGCTCACAAAGTGTATCTGT 268

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QY 301 ACAAAATAGTCAGTGTCACTATCCATGATGATTTTAAGACATGTACCAGATATG-TTA 359
Db 329 AATAATAAGTTGTGTCACTATTTATAGTACTTTATGACATGTGCCAGGTATGTTTA 388

QY 360 TGTGTGTTGGTTATACAAATAAAGTTTATTACCACCAAAAAA 410
Db 389 TGTGTGTTGGTTGTAATAATAAAGTTTACGGATATAATAGATGATAA 439

RESULT 12
A39553
LOCUS
DEFINITION Sequence 41 from Patent WO9416076.
ACCESSION A39553
VERSION A39553.1 GI:2295844
KEYWORDS
SOURCE
  ORGANISM
    unidentified
    unclassified sequences.
  REFERENCE
    1 (bases 1 to 288)
    Dubock,A.C., Powell,K.A. and Rees,S.B.
    ANTIMICROBIAL-PROTEIN-PRODUCING ENDOSYMBIOTIC MICROORGANISMS
    ZENECA LTD (GB)
    Patent: WO 9416076-A 41 21-JUL-1994;
    Other publication AU 5820494 940815.
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QY 61 GTTCTTTTGTGCTTTTGAAGCACCACCAATAGTGTGGAAGCAGCAAGTTGTGCGAAAGG 120
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QY 121 CCAAGTGGGACATGGTCAGGAGTCTGTGGAACAATAACGCAATCAGTGCATT 180
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QY 241 TGCTACTTTCTTGTGTTAAT 259
Db 268 TGCTACTTTCTTGTGTTAAT 286

RESULT 14
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LOCUS
DEFINITION Sequence 58 from patent US 6187904.
ACCESSION A130280
VERSION A130280.1 GI:14118177
KEYWORDS
SOURCE
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    Unclassified.
  REFERENCE
    1 (bases 1 to 288)
    Broekaert,W.F., Cammue,B.P.A., Osborn,R.W., Rees,S.B.,

QY 88 GTTCTTTTGTGCTTTTGAAGCACCACCAATAGTGTGGAAGCAGCAAGTTGTGCGAAAGG 147
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QY 241 TGCTACTTTCTTGTGTTAAT 259
Db 268 TGCTACTTTCTTGTGTTAAT 286

RESULT 13
A050161
LOCUS
DEFINITION Sequence 58 from patent US 5824869.
ACCESSION A050161
VERSION A050161.1 GI:5972153
KEYWORDS
SOURCE
  ORGANISM
    Unknown.
    Unclassified.
  REFERENCE
    1 (bases 1 to 288)
    Broekaert,W.F., Cammue,B.P.A., Osborn,R.W., Rees,S.B.,
    Terras,F.R.G. and Vanderleyden,J.
    Biocidal proteins
    Patent: US 5824869-A 58 20-OCT-1998;
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Db 28 GTTTATTAGTCATCGCTAAGTTTGGTCCATCATCGCACTCTTTTGTGCTCTT 87

QY 61 GTTCTTTTGTGCTTTTGAAGCACCACCAATAGTGTGGAAGCAGCAAGTTGTGCGAAAGG 120
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QY 121 CCAAGTGGGACATGGTCAGGAGTCTGTGGAACAATAACGCAATCAGTGCATT 180
Db 148 CCAAGTGGGACATGGTCAGGAGTCTGTGGAACAATAACGCAATCAGTGCATT 207

QY 181 AACCTTGAGAAAGCAGCATCGATCGATCTTGCACACTATGTCTTCCAGCTCACAAAGTGTATC 240
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RESULT 14
A130280
LOCUS
DEFINITION Sequence 58 from patent US 6187904.
ACCESSION A130280
VERSION A130280.1 GI:14118177
KEYWORDS
SOURCE
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    Unknown.
    Unclassified.
  REFERENCE
    1 (bases 1 to 288)
    Broekaert,W.F., Cammue,B.P.A., Osborn,R.W., Rees,S.B.,
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Terras,F.R.G. and Vanderleyden,J.  
Biocidal proteins  
JOURNAL  
Patent: US 6187904-A 58 13-FEB-2001;  
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Query Match 61.4%; Score 254.2; DB 6; Length 288;  
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QY 61 GTTCTTTTGGTCTTTCGAAGCACCACCAACAAATGGTGGAGCAGAGTTGTGCGAAGG 120  
DB 88 GTTCTTTTGGTCTTTCGAAGCACCACCAACAAATGGTGGAGCAGAGTTGTGCGAAGG 147  
QY 121 CCAAGTGGGACATGGTCAGGAGTCTGTGGAACCAATTAACGCATCAAGATCAGTGCATT 180  
DB 148 CCAAGTGGGACATGGTCAGGAGTCTGTGGAACCAATTAACGCATCAAGATCAGTGCATT 207  
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QY 241 TGCTACTTTCCTTTGTTAAT 259  
DB 268 TGCTACTTTCCTTTGTTAAT 286

RESULT 15

I23736 LOCUS I23736 288 bp DNA linear PAT 07-OCT-1996  
DEFINITION Sequence 58 from patent US 5538525.  
ACCESSION I23736  
VERSION I23736.1 GI:1603606  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 288)  
AUTHORS Broekaert,W.F., Cammue,B.P.A., Osborn,R.W., Rees,S.B.,  
Terras,F.R.G. and Vanderleyden,J.  
TITLE Biocidal proteins  
JOURNAL Patent: US 5538525-A 58 23-JUL-1996;  
FEATURES Location/Qualifiers  
1. .288  
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QY 61 GTTCTTTTGGTCTTTCGAAGCACCACCAACAAATGGTGGAGCAGAGTTGTGCGAAGG 120  
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QY 121 CCAAGTGGGACATGGTCAGGAGTCTGTGGAACCAATTAACGCATCAAGATCAGTGCATT 180  
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QY 241 TGCTACTTTCCTTTGTTAAT 259  
DB 268 TGCTACTTTCCTTTGTTAAT 286  
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Job time : 2310 secs

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GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

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Title: US-09-759-584-48

Perfect score: 414

Sequence: 1 GTTTATTAGTATCATGCC.....CAAAAAAAAAAAAAAAAAAAAA 414

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: Geneseq2000s.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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1	414	100.0	414	2	AAQ38650		AAQ38650 Rs-APPI C
2	414	100.0	414	2	AAQ70128		AAQ70128 Antimicro
3	414	100.0	414	2	AAT72333		AAT72333 Raphanus
4	414	100.0	414	2	AAT68696		AAT68696 Radish an
5	323.8	78.2	394	10	ADC51221		ADC51221 Brassica
6	323.8	78.2	394	13	ADU71300		ADU71300 Brassica
7	307.8	74.3	426	10	ADC51223		ADC51223 Brassica
8	307.8	74.3	426	13	ADU71302		ADU71302 Brassica
9	255	61.6	449	3	AA53190		AA53190 Raphanus
10	254.2	61.4	261	2	AAQ38652		AAQ38652 Rs-APP2 C
11	254.2	61.4	288	2	AAQ70130		AAQ70130 Antimicro
12	242.4	58.6	403	2	AAV10632		AAV10632 A. thalia
13	232.4	56.1	575	3	AAZ99339		AAZ99339 DNA encod
14	223	53.9	400	2	AAV10633		AAV10633 A. thalia
15	223	53.9	400	7	ADZ75091		ADZ75091 Arabidops
16	203.4	49.1	500	2	AAT94581		AAT94581 Composite
17	202.6	48.9	414	3	AAZ39123		AAZ39123 Wasabia j
18	201	48.6	416	3	AAZ39124		AAZ39124 Wasabia j
19	199.8	48.3	243	6	ABQ82690		ABQ82690 Wasabia j

20	199.8	48.3	243	6	ADG87728		Adg87728 A. thalia
21	199.8	48.3	243	6	ADG87923		Adg87923 A. thalia
22	199.8	48.3	243	8	ADA68378		Ada68378 Arabidops
23	198.2	47.9	243	6	ABQ82691		Abq82691 Wasabia j
24	196.6	47.5	243	6	ABZ14241		Abz14241 Arabidops
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26	196.6	47.5	243	6	ADG87824		Adg87824 A. thalia
27	196.6	47.5	243	8	ABZ42136		Abz42136 Arabidops
28	194.6	47.0	308	2	AAT94577		Aat94577 Cloned 5'
29	193.8	46.8	481	2	AAT99289		Aat99289 Alysaum s
30	180	43.5	270	2	AAT94582		Aat94582 Amplified
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32	178	43.0	1973	3	AAZ99324		Aaz99324 Arabidops
33	156.8	37.9	522	3	AAZ99327		Aaz99327 DNA encod
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36	153.6	37.1	1616	2	AAV10646		Aav10646 A. thalia
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38	152.4	36.8	534	3	AAZ99325		Aaz99325 DNA encod
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40	147.6	35.7	443	3	AAZ99330		Aaz99330 DNA encod
41	145.8	35.2	485	3	AAZ99337		Aaz99337 DNA encod
42	145.8	35.2	1093	3	AAZ99334		Aaz99334 DNA encod
43	145.4	35.1	437	3	AAZ99331		Aaz99331 DNA encod
44	145	35.0	434	3	AAZ99332		Aaz99332 DNA encod
45	144.6	34.9	488	3	AAZ99338		Aaz99338 DNA encod

## ALIGNMENTS

### RESULT 1

AAQ38650  
ID AAQ38650 standard; DNA; 414 BP.

XX AC AAQ38650;

XX DT 25-MAR-2003 (revised)

DT 07-JUL-1993 (first entry)

XX DE Rs-APPI CDNA.

XX KW Raphanus sativus; Brassica; Arabidopsis; Cnicus; Lathyrus; Clitoria;

KW fungicide; bactericide; antibiotic; antifungal; gram positive;

KW plant disease resistance; low toxicity.

XX OS Raphanus sativus.

XX FH Key Location/Qualifiers

FT CDS 16..256

FT FT /\*tag= a

XX PN WO9305153-A1.

XX PD 18-MAR-1993.

XX PF 27-AUG-1992; 92WO-GB001570.

XX PR 29-AUG-1991; 91GB-00018523.

PR 13-FEB-1992; 92GB-00003038.

XX PR 25-JUN-1992; 92GB-00013526.

XX PA (ICIL ) IMPERIAL CHEM IND PLC.

XX PI Broekaert WF, Cammue BPA, Osborn RW, Rees SB, Terras PRG;

PI Vanderleyden J;

XX DR WPT; 1993-100978/12.

XX PT Biocidal proteins isolated from seeds of plants - e.g. brassica or  
PT dahlia, useful for increasing plants' resistance to fungal and bacterial  
PT diseases.  
XX

```
PS Example 21; Fig 35; 110pp; English.
XX
CC This cDNA represents the sequence of Rs-AFP1 from Raphanus sativus. PCR
CC primer AAQ38640 was used together with AAQ38641 to generate a probe for
CC screening a Raphanus sativus seed cDNA library. This primer corresponds
CC to amino acids 2 to 7 of Rs-AFP1 and has a sense orientation. The 144bp
CC product was partially re-amplified using AAQ38642 and AAQ38641 to give a
CC 123bp product, which was further reamplified with the same primers and
CC digoxigenin-11-dUTP instead of dTTP to give a digoxigenin labeled PCR
CC product. This was used to screen a lambda ZAPII cDNA library by in situ
CC plaque hybridisation. Positive plaques were purified and subjected to two
CC additional screening rounds with the same probe. Inserts were excised in
CC vivo into the pBluescript phagemid form with the aid of helper phage
CC R408. Inserts from 22 positive clones were excised by EcoRI digestion and
CC their size compared by agarose gel electrophoresis. Four clones had
CC insert sizes of approx. 400bp the others between 250-300bp. The inserts
CC of the 4 largest clones were then sequenced and found to differ only in
CC the length of their 5' and 3' UTR's. The longest sequence is given here.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;

Query Match 100.0%; Score 414; DB 2; Length 414;
Best Local Similarity 100.0%; Pred. No. 6e-92;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTTATTAGTGCATCATGGCTAAGTTTGGTGCATCATCGCACTCTTTTTCGCTCTT 60
DB |||||||
QY 61 GTTCTTTTTCGCTCTTTCGAAGCACCACCAATGGTGAAGCAGAGAAGTTGTGCGAAGG 120
DB |||||||
QY 61 GTTCTTTTTCGCTCTTTCGAAGCACCACCAATGGTGAAGCAGAGAAGTTGTGCGAAGG 120
DB |||||||
QY 121 CCAAGTGGGACATGGTCAGGAGTCTGTGGAACAATAACGCAATGCAAGAAATCAGTGCATT 180
DB |||||||
QY 121 CCAAGTGGGACATGGTCAGGAGTCTGTGGAACAATAACGCAATGCAAGAAATCAGTGCATT 180
DB |||||||
QY 181 AACCTTGAGAACGACGACATGGATCTTGAACAATAACGCAATGCAAGTGCATT 240
DB |||||||
QY 181 AACCTTGAGAACGACGACATGGATCTTGAACAATAACGCAATGCAAGTGCATT 240
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DB |||||||
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DB |||||||

RESULT 2
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ID AAQ70128 standard; cDNA; 414 BP.
XX
XX AAQ70128;
AC
AC
DT 25-MAR-2003 (revised)
DT 14-FEB-1995 (first entry)
XX
XX Antimicrobial Rs-AFP1.
DE
DE Antimicrobial; Rs-AFP1; symbiosis; disease-resistance; fungus-resistance;
KW Clavibacter xyli subsp. cynodontis; Cxc; crop improvement; endophyte; ss.
XX
XX Raphanus sativus.
OS
XX WO9416076-A1.
XX
```

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PD 21-JUL-1994.
XX
PF 05-JAN-1994; 94WO-GB0000012.
XX
PR 08-JAN-1993; 93GB-000000281.
XX
PA (ZENE ) ZENECA LTD.
XX
XX Dubock AC, Powell KA, Rees SB;
PI
XX WPI; 1994-249223/30.
DR P-PSDB; AAR57325.
XX
XX Antimicrobial protein producing endo-symbiotic microorganisms - is
PT produced by combining nucleic acids encoding the protein with an
PT endophyte, useful for protecting plant hosts from esp. fungal disease.
XX
PS Disclosure; Page 31; 39pp; English.
XX
CC Plant-derived antimicrobial proteins are expressed in endosymbiotic
CC Clavibacter xyli subsp. cynodontis (Cxc). Plants or seeds treated with
CC recombinant Cxc are protected against fungal disease. A suitable
CC antimicrobial protein is Rs-AFP1 from R. sativus. The full-length cDNA
CC sequence of Rs-AFP1 is given in AAQ70128. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX
SQ Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;

Query Match 100.0%; Score 414; DB 2; Length 414;
Best Local Similarity 100.0%; Pred. No. 6e-92;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTTATTAGTGCATCATGGCTAAGTTTGGTGCATCATCGCACTCTTTTTCGCTCTT 60
DB |||||||
QY 1 GTTTATTAGTGCATCATGGCTAAGTTTGGTGCATCATCGCACTCTTTTTCGCTCTT 60
DB |||||||
QY 61 GTTCTTTTTCGCTCTTTCGAAGCACCACCAATGGTGAAGCAGAGAAGTTGTGCGAAGG 120
DB |||||||
QY 61 GTTCTTTTTCGCTCTTTCGAAGCACCACCAATGGTGAAGCAGAGAAGTTGTGCGAAGG 120
DB |||||||
QY 121 CCAAGTGGGACATGTCTAGGAGTCTGTGGAACAATAACGCAATGCAAGAAATCAGTGCATT 180
DB |||||||
QY 121 CCAAGTGGGACATGTCTAGGAGTCTGTGGAACAATAACGCAATGCAAGAAATCAGTGCATT 180
DB |||||||
QY 181 AACCTTGAGAACGACGACATGGATCTTGAACAATAACGCAATGCAAGTGCATT 240
DB |||||||
QY 181 AACCTTGAGAACGACGACATGGATCTTGAACAATAACGCAATGCAAGTGCATT 240
DB |||||||
QY 241 TGTACTTTCTTGTGTTAATTTATCGCAAACTCTTTCGTTGAATAGTTTATGTAATTAC 300
DB |||||||
QY 241 TGTACTTTCTTGTGTTAATTTATCGCAAACTCTTTCGTTGAATAGTTTATGTAATTAC 300
DB |||||||
QY 301 ACAAATAAGTCAGTGTCTACTATCCATGAGTGATTTTAAAGACATGTACCAGATATGTTAT 360
DB |||||||
QY 301 ACAAATAAGTCAGTGTCTACTATCCATGAGTGATTTTAAAGACATGTACCAGATATGTTAT 360
DB |||||||
QY 361 GTTGGTTCGGTTATACAAATAAAGTTTATTCACCAAAAAAAAAAAAAAAAAAAAA 414
DB |||||||
QY 361 GTTGGTTCGGTTATACAAATAAAGTTTATTCACCAAAAAAAAAAAAAAAAAAAAA 414
DB |||||||

RESULT 3
AA72333
ID AA72333 standard; cDNA; 414 BP.
XX
XX AA72333;
AC
AC
DT 25-MAR-2003 (revised)
DT 19-JAN-1998 (first entry)
XX
XX Raphanus sativus antifungal protein I (Rs-AFP1) cDNA.
DE
XX Antifungal protein; candida; fungal resistance; food additive; radish;
KW
```





QY 1 GTTTTATTAGTCATGCTAAGTTTGGTCCATCGCACTTCTTTTGGTCTCTT 60  
 DB 1 GTTTTATTAGTCATGCTAAGTTTGGTCCATCGCACTTCTTTTGGTCTCTT 60  
 QY 61 GTTCTTTTGGTCTCTTTCGAAGCACCACCAATGTTGGTGAAGCAGAGAGTTGTGCGAAAGG 120  
 DB 61 GTTCTTTTGGTCTCTTTCGAAGCACCACCAATGTTGGTGAAGCAGAGAGTTGTGCGAAAGG 120  
 QY 121 CCAAGTGGACATGTCAGAGTCTGTGGAACAATAACGCATGCAAGATCAGTGCATT 180  
 DB 121 CCAAGTGGACATGTCAGAGTCTGTGGAACAATAACGCATGCAAGATCAGTGCATT 180  
 QY 181 AACCTTGAGAAAGCAGACATGATCTGCAACTATGCTTCCAGCTCACAAGTGTATC 240  
 DB 181 AACCTTGAGAAAGCAGACATGATCTGCAACTATGCTTCCAGCTCACAAGTGTATC 240  
 QY 241 TGTACTTTTCCCTTGTAAATTTATCGCAAACTCTTTTGGTGAATAGTTTATGTAATTTAC 300  
 DB 241 TGTACTTTTCCCTTGTAAATTTATCGCAAACTCTTTTGGTGAATAGTTTATGTAATTTAC 300  
 QY 301 ACAAATAAGTCAGTGTCTACTATCCATGAGTGAATTTTAAGACATGTACAGATATGTTAT 360  
 DB 301 ACAAATAAGTCAGTGTCTACTATCCATGAGTGAATTTTAAGACATGTACAGATATGTTAT 360  
 QY 361 GTTGGTTCGGTTATACAAATAAAGTTTATTCACCAAAAAA 414  
 DB 361 GTTGGTTCGGTTATACAAATAAAGTTTATTCACCAAAAAA 414

## RESULT 5

ADCS1221  
 ID ADCS1221 standard; DNA; 394 BP.

AC ADCS1221;

DT 18-DEC-2003 (first entry)

DE Brassica oleracea defensin protein coding sequence.

XX antimicrobial protein; defensin; transgenic plant;  
 KW composite disease resistance; pathogenic bacteria;  
 KW rice white leaf blight; brown-stripe disease; glume blight;  
 KW seedling damping-off disease; filamentous fungi; rice blight;  
 KW sheath blight disease; leaf blight; gene; ds.

XX Brassica oleracea.

XX Key Location/Qualifiers

FT 1..243

FT CDS /tag= a

FT /product= "Brassica oleracea defensin protein"

XX JP2003088379-A.

XX 25-MAR-2003.

XX 18-SEP-2001; 2001JP-00283117.

XX 18-SEP-2001; 2001JP-00283117.

XX (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.

XX WPI; 2003-621123/59.

DR P-PSDB; ADCS1222.

XX Novel protein from Brassica campestris, useful as antimicrobial against  
 PT plant pathogenic filamentous fungi or pathogenic bacteria, especially for  
 PT treating e.g. rice white leaf blight and sheath blight disease.

XX Claim 3; SEQ ID NO 1; 34pp; Japanese.

XX The invention comprises the amino acid and coding sequences of

CC antimicrobial (defensin) proteins from Brassica. The DNA and protein

CC sequences of the invention are useful for producing transformed plants  
 CC with composite disease resistance, especially resistant to diseases  
 CC caused by pathogenic bacteria, such as: rice white leaf blight, brown-  
 CC stripe disease, glume blight, and seedling damping-off disease. As well  
 CC as diseases caused by filamentous fungi, such as: rice blight, sheath  
 CC blight disease, and leaf blight. The present DNA sequence encodes a  
 CC Brassica defensin protein of the invention.

SQ Sequence 394 BP; 116 A; 71 C; 82 G; 125 T; 0 U; 0 Other;

Query Match 78.2%; Score 323.8; DB 10; Length 394;  
 Best Local Similarity 90.4%; Pred. No. 8.8e-70;  
 Matches 357; Conservative 0; Mismatches 37; Indels 1; Gaps 1;

QY 16 ATGGCTAAGTTTGGCTCCATCGCACTTCTTTTGGTCTCTTCTTTTGGTCTCTTCTTTTGGTCTCTT 75

DB 1 ATGGCTAAGTTTGGTCCATCGCACTTCTTTTGGTCTCTTCTTTTGGTCTCTTCTTTTGGTCTCTT 60

QY 76 TTCTGAAGCACCACCAATGTTGGTGAAGCAGAGAGTTGTGCAAAAGGCCAAGTGGGACATGG 135

DB 61 CTCGAAGCACCACCAATGTTGGTGAAGCAGAGAGTTGTGCGAGAGGCCAAGTGGGACATGG 120

QY 136 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAAATCAGTGCATTAACTTCGAGAAAGCA 195

DB 121 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAAATCAGTGCATTAACTTCGAGAAAGCA 180

QY 196 CGACATGAGTCTTGCACACTATGCTTCCAGCTCACAAGTGTATCTGCTACTTCTCTTCTTCT 255

DB 181 CGACATGAGTCTTGCACACTATGCTTCCAGCTCACAAGTGTATCTGCTACTTCTCTTCTTCT 240

QY 256 TAAATTTATCGCAAACTCTTTTGGTGAATAGTTTATGTAATTTTACAAAAATAAGTCAGT 315

DB 241 TAACTTTATCGCAAACTCTTTTGGTGAATAGTTTATGTAATTTTACAAAAATAAGTCAGT 300

QY 316 GTCACATCCATGAGTGAATTTAAGACATGTACCGAGATGATGTTGTTGGTTCGGTTATA 375

DB 301 GTCACATCCATGAGTGAATTTAAGACATGTACCGAGATGATGTTGTTGGTTCGGTTATA 360

QY 376 CAATAAAGTTTATTCACCAAAAAA 410

DB 361 -ATATAAAGTTTATTCACCAAAAAA 394

## RESULT 6

ADU71300

ID ADU71300 standard; cDNA; 394 BP.

XX AC ADU71300;

DT 10-FEB-2005 (first entry)

XX Brassica oleracea defensin protein coding sequence - SEQ ID 1.

XX antimicrobial; plant disease resistance; gene; ss; defensin.

XX Brassica oleracea.

XX Key Location/Qualifiers

FT 1..243

FT CDS /tag= a

FT /product= "Brassica oleracea defensin protein - SEQ ID 2"

XX JP2004329215-A.

XX 25-NOV-2004.

XX 07-JUN-2004; 2004JP-00168986.

XX 18-SEP-2001; 2001JP-00283117.

XX (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.

XX WPI; 2004-809169/80.

```
DR P-PSDB; ADU71301.
XX
XX Novel Brassica sp. derived protein having antimicrobial activity, useful
XX for producing multiple disease resistant plants.
XX
XX Example 2; SEQ ID NO 1; 16pp; Japanese.
XX
XX The invention comprises the amino acid and coding sequence of an
XX antimicrobial protein obtained from Brassica sp. The DNA and protein
XX sequences of the invention are useful in the production of a multiple
XX disease resistant plant. The present cDNA sequence encodes the Brassica
XX oleracea defensin protein.
XX
XX Sequence 394 BP; 116 A; 71 C; 82 G; 125 T; 0 U; 0 Other;
XX
XX
XX Query Match 78.2%; Score 323.8; DB 13; Length 394;
XX Best Local Similarity 90.4%; Pred. No. 8.8e-70;
XX Matches 357; Conservative 0; Mismatches 37; Indels 1; Gaps 1;
XX
XX QY 16 ATGGCTAAGTTTGGTCCATCATCGCACTTCTTTTGTGCTCTTGTCTTTTGTCTGCT 75
XX Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 1 ATGGCTAAGTTTGGTCCATCATCGCACTTCTTTTGTGCTCTTGTCTTTTGTCTGCT 60
XX
XX QY 76 TTCGAAGCACCACAAATGTTGGAAGCAGAGAAGTTGTGCAAGGCCCAAGTGGACATGG 135
XX Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 61 CTCGAAGCACCACAAATGTTGGAAGCAGAGAAGTTGTGCAAGGCCCAAGTGGACATGG 120
XX
XX QY 136 TCAGAGTCTGTGGAACCAATAACGCATCGCAAGATCAGTGCATTAACCTTGAGAAAGCA 195
XX Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 121 TCAGAGTCTGTGGAACCAATAACGCATCGCAAGATCAGTGCATTAACCTTGAGAAAGCA 180
XX
XX QY 196 CGACATGGATCTTGGCAATATGCTCTTCCAGCTCACAAGTGTATCTGTACTTCTTGT 255
XX Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 181 CGACATGGATCTTGGCAATATGCTCTTCCAGCTCACAAGTGTATCTGTACTTCTTGT 240
XX
XX QY 256 TAAATTTATCGCAAACTCTTGTGTAATAGTATTTATGTAATTTACAAAAAAGTCAGT 315
XX Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 241 TAACTTATGCGCAAACTCTTGTGTAATAGTATTTATGTAATTTACAAAAAAGTCAGT 300
XX
XX QY 316 GTCACATCCATGAGTGAATTTAAGACATGTACC--AGATATGTTATGTTGGTTCGGTTA 373
XX Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 301 GTCACATCAATGAGTGAATTTATGACATGTACCTGATATATGTTATGTTGGTTCGGTTA 360
XX
XX QY 374 TACAATAAAGTTTATTCACCAAAAAA 414
XX Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 361 TA-ATAAAGTTTATGACCGTTTCAAAAAA 400
XX
XX
XX RESULT 8
XX ADU71302
XX ID ADU71302 standard; DNA; 426 BP.
XX
XX AC ADU71302;
XX
XX DT 10-FEB-2005 (first entry)
XX
XX DE Brassica antimicrobial protein coding sequence - SEQ ID 3.
XX
XX KW antimicrobial; plant disease resistance; gene; ds.
```

```
XX OS Brassica sp.
XX FH Key Location/Qualifiers
XX CDS 1..243
FT /tag= a
FT /product= "Brassica antimicrobial protein - SEQ ID 4"
XX
XX JP2004329215-A.
XX
XX PD 25-NOV-2004.
XX
XX PF 07-JUN-2004; 2004JP-00168986.
XX
XX PR 18-SEP-2001; 2001JP-00283117.
XX
XX PA (DOKU-) DOKURITSU GYOSEI HOJIN NOGOIN NOGYO SEIBUTSU SH.
XX
XX DR WPI; 2004-809169/80.
XX
XX DR P-PSDB; ADU71303.
XX
XX PT Novel Brassica sp. derived protein having antimicrobial activity, useful
XX for producing multiple disease resistant plants.
XX
XX PS Claim 3; SEQ ID NO 3; 16pp; Japanese.
XX
XX CC The invention comprises the amino acid and coding sequence of an
XX antimicrobial protein obtained from Brassica sp. The DNA and protein
XX sequences of the invention are useful in the production of a multiple
XX disease resistant plant. The present DNA sequence encodes the Brassica
XX antimicrobial protein of the invention.
XX
XX SQ Sequence 426 BP; 142 A; 72 C; 84 G; 128 T; 0 U; 0 Other;

Query Match 74.3%; Score 307.8; DB 13; Length 426;
Best Local Similarity 88.8%; Pred. No. 7.6e-66;
Matches 356; Conservative 0; Mismatches 42; Indels 3; Gaps 2;

QY 16 ATGGCTAAGTTGCGTCCATCATCGCACTCTTTTGGCTGCTGCTTTTGGTCTGCT 75
DB 1 ATGGCCCAAGTTTGTGCTATCATTTGCCCACTTTTGGCTGCTTGTCTTTTAGCTGCT 60

QY 76 TTCGAAGCACCAACATGTGTGAAGCACAGAAAGTTGTGCGAAGGCCAAGTGGGACATGG 135
DB 61 TTCGAGCCACCAACATGTGTGAAGCACAGAAAGTTGTGCGAAGGCCAAGTGGGACATGG 120

QY 136 TCAGGAGTCTGTGGAAACAATAACGCATCAAGAAATCAGTGCATTAACTTGAGAAAGCA 195
DB 121 TCAGGAGTCTGTGGAAACAATAACGCATCAAGAAATCAGTGCATTAACTTGAGAAAGCA 180

QY 196 CGACATGGATCTTGGAACTATGCTTCCAGCTCACAAGTGATCTGCTACTTTCCTTGT 255
DB 181 CGACATGGATCTTGGAACTATGCTTCCAGCTCACAAGTGATTTTGTACTTCCCTTGT 240

QY 256 TAAATTTATCGCAACTCTTTGGTGAATAGTTTATGTAATTTACACAAATAAAGTCAGT 315
DB 241 TAACTTATGCGCAACTCTTTGGTGAATAGTTTATGTAATTTACACAAATAAAGTCAGT 300

QY 316 GTCACATATCCATGAGTGAATTTTAAGACATGTACC--AGATATGTTATGTTGGTTCGGTTA 373
DB 301 GTCACATATCAATGAGTGAATTTTATGACATGTACTCATATATGTTATGTTGGTTCGGTTA 360

QY 374 TACAAATAAAGTTTATTCACCAAAAAAAAAAAAAAAAAAAAA 414
DB 361 TA-ATAAAAAGTTTATGACCCGTTCCAAAAAATAAAAAAAAAAAAA 400

RESULT 9
AA53190
ID AA53190 standard; DNA; 449 BP.
XX
XX AA53190;
XX
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```
DT 06-OCT-2000 (first entry)
XX
XX DE Raphanus sativus antibacterial protein radishin encoding DNA SEQ ID NO:1.
XX
XX KW Raphanus sativus; antibacterial; plant; resistance; paddy; radishin;
XX pathogenic microbe; radish; rice blast disease; ds.
XX
XX OS Raphanus sativus.
XX
XX FN JP2000116379-A.
XX
XX PD 25-APR-2000.
XX
XX PF 09-OCT-1998; 98JP-00288472.
XX
XX PR 09-OCT-1998; 98JP-00288472.
XX
XX PA (TOYA-) TOYAMA KEN.
XX
XX DR WPI; 2000-389821/34.
XX
XX DR P-PSDB; AAY91117.
XX
XX PT Isolated DNA from Raphanus sativus used to transform a microbe and a
XX plant to produce an antibacterial protein used to increase resistance of
XX rice paddy against pathogenic microbes.
XX
XX PS Claim 1; Page 4; 7pp; Japanese.
XX
XX CC The present sequence encodes an antibacterial protein, designated
XX radishin, isolated from Raphanus sativus (radish). A phage or plasmid
XX comprising radishin can be used for increasing resistance of paddy and
XX rice blast disease against pathogenic microbes
XX
XX SQ Sequence 449 BP; 126 A; 78 C; 94 G; 151 T; 0 U; 0 Other;

Query Match 61.6%; Score 255; DB 3; Length 449;
Best Local Similarity 81.0%; Pred. No. 7.4e-53;
Matches 333; Conservative 0; Mismatches 74; Indels 4; Gaps 3;

QY 4 TTATAGTAGATCATGGCTAAGTTTGGTCCCATCATCGCACTTCTTTTGGCTGCTCTTGT 63
DB 29 TTAGTAGTAGATCATGGCTAAGTTTGGTCCCATCATCGCACTTCTTTTGGCTGCTCTTGT 88

QY 64 CTTTGTGCTGCTTTCGAAGCACCAACAATGGTGAAGCACAGAAAGTTGTGCGAAAGGCCA 123
DB 89 GTTGTGCTGCTTTCGAAGCACCAACAATGGTGAAGCACAGAAAGTTGTGTCAGAGGCCA 148

QY 124 AGTGGGACATGGTTCAGGAGTCTGTGGAACAATAACGCATCAAGAAATCAGTGCATTAA 183
DB 149 AGTGGGACATGGTTCAGGAGTCTGTGGAACAATAACGCATCAAGAAATCAGTGCATTAA 208

QY 184 CTTGAGAAAGCAGCATGGATCTTGCACATATGCTTCCAGCTCACAAGTGTATCTGC 243
DB 209 CTTGAGAAAGCAGCATGGGCTTTCGCACTATGCTTCCAGCTCACAAGTGTATCTGT 268

QY 244 TACTTTTCTTGTAAAT--TATCGCAAACTCTTTGGTGAATAGTTT--TTATGTAATTTAC 300
DB 269 TATTTCCCTTGTAAATTCATTAACCTCTTCGGTGGTTAATAGTGGCGCATTTTACATAT 328

QY 301 ACAAAATAGTCAGTGTCTACTATCCATGATGATGATTTAAGACATGTACAGATATG-TTA 359
DB 329 AATTAATAAGTTTGTGTCACTATTATTATTAGTCACTTTATGACATGTGCGCAGGTATCTGTA 388

QY 360 TGTGTGTTGGTTATACAAATAAAGTTTATTACCACCAAAAAAAAAAAAA 410
DB 389 TGTGTGTTGGTTGTAATAATAAAAAAGTTTACCGATATAATAAGATGATAA 439

RESULT 10
AAQ38652
ID AAQ38652 standard; DNA; 261 BP.
XX
XX AAQ38652;
XX
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XX 25-MAR-2003 (revised)
DT 07-JUL-1993 (first entry)
XX
XX Rs-APP2 cDNA.
XX
XX Raphanus sativus; Brassica; Arabidopsis; Cnicus; Lathyrus; Clitoria;
KW fungicide; bacteriocide; antibiotic; antifungal; gram positive;
KW plant disease resistance; low toxicity.
XX
XX Raphanus sativus.
XX
XX Key Location/Qualifiers
FH CDS 16..256
FT /*tag= a
XX
XX WO9305153-A1.
XX
XX 18-MAR-1993.
XX
XX 27-AUG-1992; 92WO-GB001570.
XX
XX 29-AUG-1991; 91GB-00018523.
XX
XX 13-FEB-1992; 92GB-00003038.
XX
XX 25-JUN-1992; 92GB-00013526.
XX
XX (ICIL ) IMPERIAL CHEM IND PLC.
XX
XX Broekaert WF, Cammue BPA, Osborn RW, Rees SB, Terras PRG;
PI Vanderleyden J;
XX
XX WPI; 1993-100978/12.
XX
XX Biocidal proteins isolated from seeds of plants - e.g. brassica or
XX dahlia, useful for increasing plants' resistance to fungal and bacterial
XX diseases.
XX
XX Example 21; Fig 35; 110pp; English.
XX
XX This cDNA represents the sequence of Rs-APP2 from Raphanus sativus. PCR
XX primer AAQ38640 was used together with AAQ38641 to generate a probe for
XX screening a Raphanus sativus seed cDNA library. This primer corresponds
XX to amino acids 2 to 7 of Rs-APP1 and has a sense orientation. The 144bp
XX product was partially re-amplified using AAQ38642 and AAQ38641 to give a
XX 123bp product, which was further reamplified with the same primers and
XX digoxigenin-11-dUTP instead of dTTP to give a digoxigenin labeled PCR
XX product. This was used to screen a lambda ZAPII cDNA library by in situ
XX plaque hybridisation. Positive plaques were purified and subjected to two
XX additional screening rounds with the same probe. Inserts were excised in
XX vivo into the pBluescript phagemid form with the aid of helper phage
XX R408. Inserts from 22 positive clones were excised by EcoRI digestion and
XX their size compared by agarose gel electrophoresis. Four clones had
XX insert sizes of approx. 400bp the others between 250-300bp. The inserts
XX of the 4 largest clones were then sequenced and found to differ only in
XX the length of their 5' and 3' UTR's. The longest sequence was identified
XX as Rs-APP1 (AAQ38650). Rs-APP2 was seen to differ by only 2 amino acids
XX from Rs-APP1, so the Rs-APP1 cDNA was transformed to the Rs-APP2
XX nucleotide sequence by PCR assisted site directed mutagenesis. (Updated
XX on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 261 BP; 67 A; 55 C; 59 G; 80 T; 0 U; 0 Other;
SQ
Query Match 61.4%; Score 254.2; DB 2; Length 261;
Best Local Similarity 98.8%; Pred. No. 1e-52;
Matches 256; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GTTTATTAGTGCATGCGCTAAGTTTGGTCCCATCGCACTTCTTTTGTGCTCTT 60
DB 1 GTTTATTAGTGCATGCGCTAAGTTTGGTCCCATCGCACTTCTTTTGTGCTCTT 60
QY 61 GTTCTTTTGTGCTTTTGAAGCACCACCAATGGTGGGAAGCAGAGAGTTGTGCAAGG 120
DB 61 GTTCTTTTGTGCTTTTGAAGCACCACCAATGGTGGGAAGCAGAGAGTTGTGCAAGG 147

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QY 121 CCAAGTGGGACATGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATT 180
DB 121 CCAAGTGGGACATGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATT 180
QY 181 AACCTTGAGAAAGCAGCAGCATGGATCTTGGCAACTATGTCTTCCAGCTCACAAGTGTATC 240
DB 181 AGACTTGAGAAAGCAGCAGCATGGATCTTGGCAACTATGTCTTCCAGCTCACAAGTGTATC 240
QY 241 TGTACTTTTCTTGTGTTAAT 259
DB 241 TGTACTTTTCTTGTGTTAAT 259
RESULT 11
AAQ70130
ID AAQ70130 standard; cDNA; 288 BP.
XX
XX AC AAQ70130;
XX
XX 25-MAR-2003 (revised)
DT 14-FEB-1995 (first entry)
XX
XX DE Antimicrobial Rs-APP2.
XX
XX KW Antimicrobial; Rs-APP2; symbiosis; disease-resistance; fungus-resistance;
KW Clavibacter xyli subsp. cynodentis; Cxc; crop improvement; endophyte;
KW PCR; polymerase chain reaction; mutagenesis; ss.
XX
XX OS Raphanus sativus.
XX
XX PN WO9416076-A1.
XX
XX PD 21-JUL-1994.
XX
XX PF 05-JAN-1994; 94WO-GB0000012.
XX
XX PR 08-JAN-1993; 93GB-00000281.
XX
XX PA (ZENE ) ZENECA LTD.
XX
XX PI Dubock AC, Powell KA, Rees SB;
XX
XX DR WPI; 1994-249223/30.
XX
XX P-PSDB; AAR57327.
XX
XX PT Antimicrobial protein producing endo-symbiotic microorganisms - is
XX produced by combining nucleic acids encoding the protein with an
XX endophyte, useful for protecting plant hosts from esp. fungal disease.
XX
XX PS Disclosure; Page 33; 39pp; English.
XX
XX CC Plant-derived antimicrobial proteins are expressed in endosymbiotic
XX Clavibacter xyli subsp. cynodentis (Cxc). Plants or seeds treated with
XX recombinant Cxc are protected against fungal disease. A suitable
XX antimicrobial protein is Rs-APP1 from R. sativus. The full-length cDNA
XX sequence of PCR assisted site-directed mutagenesis of Rs-APP2 is given in
XX CC AAQ70130 and the deduced amino acid sequence in AAR57327. (Updated on 25-
XX MAR-2003 to correct PN field.)
XX
XX SQ Sequence 288 BP; 70 A; 66 C; 69 G; 83 T; 0 U; 0 Other;
Query Match 61.4%; Score 254.2; DB 2; Length 288;
Best Local Similarity 98.8%; Pred. No. 1e-52;
Matches 256; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GTTTATTAGTGCATGCGCTAAGTTTGGTCCCATCGCACTTCTTTTGTGCTCTT 60
DB 28 GTTTATTAGTGCATGCGCTAAGTTTGGTCCCATCGCACTTCTTTTGTGCTCTT 87
QY 61 GTTCTTTTGTGCTTTTGAAGCACCACCAATGGTGGGAAGCAGAGAGTTGTGCAAGG 120
DB 88 GTTCTTTTGTGCTTTTGAAGCACCACCAATGGTGGGAAGCAGAGAGTTGTGCAAGG 147

```

QY 121 CCAAGTGGACATGGTCAGAGTCTGTGGAACAATAACGCATGCAAGAATCAGTGCATT 180  
Db 148 CCAAGTGGACATGGTCAGAGTCTGTGGAACAATAACGCATGCAAGAATCAGTGCATT 207  
QY 181 AACCTTTGAGAAAGCAGCATGATCTTGCACACTATGTCTTCCAGCTCACAAGTGTATC 240  
Db 208 AGACTTGAGAAAGCAGCATGATCTTGCACACTATGTCTTCCAGCTCACAAGTGTATC 267  
QY 241 TGCTACTTTCCTTGTAAAT 259  
Db 268 TGCTACTTTCCTTGTAAAT 286

## RESULT 12

AAV10632

ID AAV10632 standard; DNA; 403 BP.

XX

AC AAV10632;

XX 23-JUN-1998 (first entry)

XX A. thaliana PDF1.1 DNA.

XX

XX Defense; PDF1.1; protection; plant; pathogen; jasmonate; ethylene;

XX fungi; ss.

XX

XX Arabidopsis thaliana.

XX

XX Key Location/Qualifiers

FH CDS 26..268

FT /\*tag= a

FT sig\_peptide 26..113

FT /\*tag= b

FT mat\_peptide 114..265

FT /\*tag= c

FT /product= "PDF1.1"

FT /note= "plant defensin"

XX

XX WO9800023-A2.

XX

XX 08-JAN-1998.

XX

XX 20-JUN-1997; 97WO-GB001672.

XX

XX 01-JUL-1996; 96GB-00013753.

XX

XX (ZENE ) ZENECA LTD.

XX

XX Broekaert WF, Thomma BPHJ, Penninckx IAMA, Terras PRG, Manners JM;

XX Kazan K;

XX

XX WPI; 1998-086663/08.

XX P-PSDB; AAW40345.

XX

XX Protecting plants against pathogens by inducing defensin genes - by

XX stimulating ethylene or jasmonate pathways, also new promoter of defensin

XX Gene from Arabidopsis.

XX

XX Disclosure; Fig 1; 72pp; English.

XX

XX This sequence encodes the Arabidopsis PDF1.1 gene which is used in a

XX novel method for the protection of plants against pathogens which

XX involves inducing expression of a plant defensin gene by stimulating the

XX jasmonate and/or ethylene pathways. The method is used to induce

XX protection against necrotrophic pathogens, specifically fungi and does

XX not require cytotoxic or potentially harmful chemicals

XX

XX Sequence 403 BP; 112 A; 77 C; 85 G; 129 T; 0 U; 0 Other;

XX

XX Query Match 58.6%; Score 242.4; DB 2; Length 403;

XX Best Local Similarity 76.5%; Pred. No. 9e-50;

XX Matches 297; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

QY 1 GTTTATTAGTATCATGGCTAAGTTTGGTCCATCATCGCACCTTCTTTTGGCTGCTCTT 60  
Db 11 GTATATAACATAGTATGCTAGTCTGCTACCATGTTACTCTTTTCTTGGCTGCTCTT 70  
QY 61 GTTCTTTTGTGCTTTTCCAAAGCACCAACAATGGTGGAAAGCACAGAAGTTGTGCGAAGG 120  
Db 71 GTTTTCTTTTGTGCTCTTTGAAAGCACCGATGGTGGTGGAAAGCACAGAAGTTGTGCGAGAGG 130  
QY 121 CCAAGTGGACATGGTCAGAGTCTGTGGAACAATAACGCATGCAAGAATCAGTGCATT 180  
Db 131 CCAAGTGGACATGGTCAGAGTCTGTGGAACAATAACGCATGCAAGAATCAGTGCATT 190  
QY 181 AACCTTTGAGAAAGCAGCATGATCTTGCACACTATGTCTTCCAGCTCACAAGTGTATC 240  
Db 191 AACCTTTGAGAAAGCAGCATGATCTTGCACACTATGTCTTCCAGCTCACAAGTGTATC 250  
QY 241 TGCTACTTTCCTTGTAAATTTATCGCAAACTCTTTTGGTGAATAGTTTTTATGTAAATTTAC 300  
Db 251 TGCTACTTTCCTTGTAAATTTATCGCAAACTCTTTTGGTGAATAGTTTTTATGTAAATTTAC 310  
QY 301 ACAAAATAGTCAGTGTCACTATCCATGAGTGAATTTAAGACATGTACCAGATGTTAT 360  
Db 311 CTATTAAATAAAGTATGTCTCACTCTATGAGAGGCTCTTATGACATGTACCAGATGTTAT 370  
QY 361 GTTGGTTCGGTTATACAAATAAAGTTTT 388  
Db 371 GTTGGTTCGGTTATACAAATAAAGTTTT 398

## RESULT 13

AAZ99339

ID AAZ99339 standard; DNA; 575 BP.

XX

AC AAZ99339;

XX

XX 03-JUL-2000 (first entry)

XX

XX DNA encoding a fusion protein of DmAMP1 and RsAPP2.

XX

XX Antimicrobial protein; AMP1; transgenic plant; linker peptide;

XX protein expression; plant defensin; RsAPP2; antifungal protein; AFP2; ss.

XX

XX Synthetic.

XX Dahlia merckii.

XX Unidentified.

XX

XX Key Location/Qualifiers

FH CDS 3..566

FT /\*tag= a

FT /product= "fusion protein of DmAMP1 and RsAPP2"

XX

XX WO200011175-A1.

XX

XX 02-MAR-2000.

XX

XX 17-AUG-1999; 99WO-GB002716.

XX

XX 18-AUG-1998; 98GB-00018001.

XX 04-DEC-1998; 98GB-00026753.

XX

XX (ZENE ) ZENECA LTD.

XX

XX Broekaert WF, Francois IEJA, De Bolle MFC, Evans IJ, Ray JA;

XX WPI; 2000-246564/21.

XX P-PSDB; AAY84072.

XX

XX Improving expression of polyproteins in plants involves coexpression of

XX two or more proteins in plants within a single transcription unit.

XX Disclosure; Fig 34; 151pp; English.

XX

CC The present sequence encodes a protein of the invention, comprising the  
CC mature proteins of the plant defensins, the Dahlia antimicrobial protein  
CC (AMP) 1 and the antifungal protein 2 (RsAFP2), linked by a linker  
CC propeptide of the invention. The specification describes methods for  
CC improving expression levels of one or more proteins in a transgenic  
CC plant. The method comprises inserting a DNA sequence having a promoter  
CC region operably linked to two or more protein encoding regions separated  
CC by a DNA sequence coding for a linker propeptide and a terminator region.  
CC The method is used to produce proteins in plants. The linker propeptide  
CC comprising a cleavage site, whereby the expressed polypeptide is post-  
CC translationally processed into the component protein molecules. The  
CC propeptide sequence is rich in amino acids A, V, S and T and contains  
CC dipeptidic sequences consisting of either two acidic, two basic or one  
CC acidic and one basic residue as a cleavable linker sequence  
XX  
XX  
SQ Sequence 575 BP; 133 A; 137 C; 149 G; 156 T; 0 U; 0 Other;

Query Match 56.1%; Score 232.4; DB 3; Length 575;  
Best Local Similarity 95.6%; Pred. No. 2.8e-47;  
Matches 239; Conservative 0; Mismatches 11; Indels 0; Gaps 0;  
QY 10 GTGATCATGGCTAAGTTGGTCCATCATCGCACTTCTTTTGGCTGCTCTTGTCTTTT 69  
DB 318 GGGCCATGGCTAAGTTGGTCCATCATCGCACTTCTTTTGGCTGCTCTTGTCTTTT 377  
QY 70 GCTGCTTTTCCAGCACCAACAATGGTGAAGCACAGAACTTGTGCGAAAGGCCAAGTGG 129  
DB 378 GCTGCTTTTCCAGCACCAACAATGGTGAAGCACAGAACTTGTGCGAAAGGCCAAGTGG 437  
QY 130 ACATGCTCAGGAGTCTGTGGAACAATACGCAATGCAAGTCAAGTCACTTGA 189  
DB 438 ACATGCTCAGGAGTCTGTGGAACAATACGCAATGCAAGTCAAGTCACTTGA 497  
QY 190 AAGACGACATGGATCTTGGCAACTATGCTTCCAGCTCACAAGTGTATCTGCTACTTT 249  
DB 498 AAGACGACATGGATCTTGGCAACTATGCTTCCAGCTCACAAGTGTATCTGCTACTTT 557  
QY 250 CCTTGTGAAT 259  
DB 558 CCTTGTGAAT 567

RESULT 14  
AAV10633  
ID AAV10633 standard; DNA; 400 BP.  
XX  
AC AAV10633;  
XX  
XX 23-JUN-1998 (first entry)  
XX  
XX A. thaliana PDF1.2 DNA.  
XX  
XX Defensin; PDF1.2; protection; plant; pathogen; jasmonate; ethylene;  
KW fungi; ss.  
XX  
XX Arabidopsis thaliana.

Key Location/Qualifiers  
CDS 32..274  
FT /\*tag= a  
FT sig\_peptide 32..119  
FT /\*tag= b  
FT mat\_peptide 120..271  
FT /\*tag= c  
FT /product= "PDF1.2"  
FT /note= "Plant defensin"

XX  
XX WO9800023-A2.  
XX  
XX 08-JAN-1998.  
XX  
XX 20-JUN-1997; 97WO-GB001672.  
XX

PR 01-JUL-1996; 96GB-00013753.  
XX  
XX (ZENE ) ZENECA LTD.  
XX  
XX Broekaert WF, Thomma BPHJ, Penninckx IAWA, Terras FRG, Manners JM;  
XX Kazan K;  
XX  
XX WPI; 1998-086663/08.  
XX P-PSDB; AAW40346.  
XX  
XX Protecting plants against pathogens by inducing defensin genes - by  
XX stimulating ethylene or jasmonate pathways, also new promoter of defensin  
XX gene from Arabidopsis.  
XX  
XX Disclosure; Fig 1; 72pp; English.  
XX  
XX This sequence encodes the Arabidopsis PDF1.2 gene which is used in a  
XX novel method for the protection of plants against pathogens which  
XX involves inducing expression of a plant defensin gene by stimulating the  
XX jasmonate and/or ethylene pathways. The method is used to induce  
XX protection against necrotrophic pathogens, specifically fungi and does  
XX not require cytotoxic or potentially harmful chemicals  
XX  
XX Sequence 400 BP; 109 A; 82 C; 80 G; 125 T; 0 U; 4 Other;  
SQ  
Query Match 53.9%; Score 223; DB 2; Length 400;  
Best Local Similarity 79.9%; Pred. No. 5.2e-45;  
Matches 274; Conservative 0; Mismatches 67; Indels 2; Gaps 1;  
QY 5 TATTAGTATCATGGCTAAGTTGGTCCATCATCGCACTTCTTTTGGCTGCTCTTGTTC 64  
DB 21 TAATAATCATCATGGCTAAGTTGGTCCATCATCGCACTTCTTTTGGCTGCTCTTGTTC 80  
QY 65 TTTTGTGCTTTTCCAGCACCAACAATGGTGAAGCACAGAACTTGTGCGAAAGGCCAA 124  
DB 81 TCTTTGTGCTTTTCCAGCACCGGCAATGGTGAAGCACAGAACTTGTGCGAAAGGCCAA 140  
QY 125 GTGGGACATGCTCAGGAGTCTGTGGAACAATACGCAATGCAAGTCAAGTCACTTAAACC 184  
DB 141 GTGGGACATGCTCAGGAGTCTGTGGAACAATGCAAGTCAAGTCACTTAAACC 200  
QY 185 TTGAGAAAGCAGCAGATGATCTTCCAACTATGCTTCCAGCTCACAAGTGTATCTGCT 244  
DB 201 TTGAGAGGAGCCAAACATGATCATGCAACTATGCTTCCAGCAGCACAAGTGTATCTGTT 260  
QY 245 ACTTTCTTGTAAATTTATCGCAACTCTTTGCGAAGTGTATGTTTATGTAATTTACACAA 304  
DB 261 ACGTCCCATGTTAAATCTACCACTAATCTTTGGTGTAAATCGTGTGTTATTTACATAAA 320  
QY 305 AATAAGTCAGTGTCACTATCCATGAGTGAATTTTAAAGACATGTA 347  
DB 321 AATAAGTCNCTGTCTAC--TCNTGAGTAACTTTATGACATGCA 361  
RESULT 15  
ADZ75091  
ID ADZ75091 standard; DNA; 400 BP.  
XX  
XX AC ADZ75091;  
XX  
XX 30-JUN-2005 (first entry)  
XX  
XX Arabidopsis leaf-specific open reading frame, SEQ ID 607.  
XX  
XX Arabidopsis  
KW Crop improvement; gene; ds; plant; plant disease; plant fungal disease;  
KW drought resistance; herbicide resistance; insect resistance;  
KW abiotic stress tolerance; salt tolerance; heat tolerance; cold tolerance;  
KW gene expression; food.  
XX  
XX Arabidopsis thaliana.  
XX  
XX WO200198480-A2.  
XX

27-DEC-2001.

22-JUN-2001; 2001WO-IB001104.

23-JUN-2000; 2000US-0213848P.

23-JUN-2000; 2000US-0214087P.

29-DEC-2000; 2000US-0258692P.

(SYGN ) SYNGENTA PARTICIPATIONS AG.

Budworth P, Brown D, Chang H, Zhu T, Han B, Wang X, Cooper B;

WPI; 2002-055861/07.

Promoters for root-specific, leaf-specific or constitutive regulation of plant gene expression, useful for regulating the expression of selected transgenes (e.g. stress tolerance and defence related genes) in economically important plants.

Disclosure; SEQ ID NO 607; 290pp; English.

The invention relates to promoters for root-specific, leaf-specific or constitutive regulation of plant gene expression. Also included are an isolated polynucleotide (N1) comprising a plant nucleotide sequence that directs root-specific transcription of an operatively linked nucleic acid segment in a plant cell, where the plant nucleotide sequence is from a gene encoding a polypeptide that is substantially similar to a polypeptide encoded by an Arabidopsis gene comprising a promoter selected from AD274492-AD274542, AD275008-AD275016 or AD275026-AD275034 or a polypeptide encoded by a rice gene comprising a promoter selected from AD275309 and AD275327, an isolated polynucleotide (N2) comprising a plant nucleotide sequence that directs constitutive transcription of an operatively linked nucleic acid segment in a plant cell, where the plant nucleotide sequence is from a gene encoding a polypeptide that is substantially similar to a polypeptide encoded by an Arabidopsis gene comprising a promoter selected from AD275007, AD275035-AD275069, AD275310-AD275326 and AD275328-AD275359), an isolated polynucleotide (N3) comprising a plant nucleotide sequence that directs leaf-specific transcription of an operatively linked nucleic acid segment in a plant, where the plant nucleotide sequence is from a gene encoding a polypeptide that is substantially similar to a polypeptide encoded by an Arabidopsis gene comprising a promoter selected from AD275177-AD275257, a recombinant vector comprising N1-N3, an expression cassette comprising N1-N3 operatively linked to an open reading frame, a recombinant vector comprising the above expression cassette, a host cell comprising the expression cassette, a plant cell containing the expression cassette, a transformed plant (the genome of which is augmented with the expression cassette), a transformed plant comprising transformed plant cells (where the cells contain the expression cassette), a method (M1) for augmenting a plant genome, a method (M2) to identify a gene having a promoter (the expression of which is altered in root), a method (M3) to identify a gene having a promoter (the expression of which is constitutive in a plant cell), a method (M4) to identify a gene having a promoter (the expression of which is altered in leaves of a plant), and a method to alter the phenotype of a plant cell comprising introducing the expression cassette. For the expression cassette, the open reading frame is from an insect resistance gene, a bacterial disease resistance gene, a fungal disease resistance gene, a viral disease resistance gene, a nematode disease resistance gene, a herbicide resistance gene, a stress resistance gene, a gene affecting grain composition or quality, a nutrient utilization gene, a mycotoxin reduction gene, a male sterility gene, a selectable marker gene, a screenable marker gene, a negative selectable marker, a gene affecting plant agronomic characteristics, or an environment or stress resistance gene. The stress resistance gene confers resistance or tolerance to drought, heat, chilling, freezing, excessive moisture, excessive salt, or excessive oxidative stress. The promoters are useful for regulating the expression of selected transgenes in economically important plants. For example, root-specific promoters may be useful for expressing defence-related genes, including those conferring insecticidal resistance and stress tolerance genes, e.g., salt, cold or drought tolerance, and genes for altering nutrient uptake, and leaf-specific promoters may be useful for producing large quantities of protein, for expressing oils or

proteins of interest, and genes for increasing the nutritional value of plant. Constitutive promoters are useful for expressing a wide variety of genes including those which alter metabolic pathways, confer disease resistance, for protein production, e.g., antibody production, or to improve nutrient uptake. The present sequence is an open reading frame from an Arabidopsis leaf specific promoter gene of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published pct sequences

SQ	Sequence	400 BP;	109 A;	82 C;	80 G;	125 T;	0 U;	4 Other;
	Query Match	53.9%;	Score	223;	DB	7;	Length	400;
	Best Local Similarity	79.9%;	Pred. No.	5.2e-45;				
	Matches	274;	Conservative	0;	Mismatches	67;	Indels	2;
	Gaps	1;						
Qy	5	TATTAGTGCATCGCTAAGTTTGGGTCATCGACTCTCTTTTCTGCTCTGTTGC	64					
Db	21	TAATAATCATCATGGCTAAGTTTGTCTTCATCATCACCTTATCTTCGCTGCTCTGTTTC	80					
Qy	65	TTTTTTGTGCTCTTCGAAAGCACCAACAATGGTGGGAAGCACAGAAAGTTGTGCGAAAGGCCAA	124					
Db	81	TCITTTGTGCTTTTCGACGCACCGGCATGGTGGGAAGCACAGAAAGTTGTGCGAAGAGCCAA	140					
Qy	125	GTGGGACATGTCAGGAGTCTGTGGAAAACAATAACGCAATGCAAGAAATCAGTGCAATTAACC	184					
Db	141	GTGGGACATGTCAGGGGTTTTCGCGAAAACAGTAATGCAATGCAAGAAATCAGTGCAATTAACC	200					
Qy	185	TTGGAAGACGACATCGATCTTGGCACTATGCTTCCAGCTCACAAGTGCTATCTGCT	244					
Db	201	TTGAAGAGCCAAACATGGATCTGCAACTATGCTTCCAGCACCAAGTGATCTGTT	260					
Qy	245	ACTTTCTCTGTTTAATTTATCGCAAACTCTTTGGTGAATAGTTTTTATGTAATTTACACAA	304					
Db	261	ACGTCCCATGTTAAATCTTACCACTAACTCTTTGGTGTAAATCGTGTGATTTTACATAA	320					
Qy	305	AATAAGTCAGTGTGCATATCCATCATGATGATTTTAAGACATGTA	347					
Db	321	AATAAGTCTGTCAC--TCNTGAGTAACCTTATGACATGCA	361					

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GenCore version 5.1.8  
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Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

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Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 2: gb\_est2.\*
- 3: gb\_est3.\*
- 4: gb\_hic.\*
- 5: gb\_est4.\*
- 6: gb\_est5.\*
- 7: gb\_est6.\*
- 8: gb\_est7.\*
- 9: gb\_gss1.\*
- 10: gb\_gss2.\*
- 11: gb\_gss3.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	327.6	79.1	484	7	CN726241 3ETMS UP
2	326.8	78.9	547	7	CN726625 3ETMS UP
3	326	78.7	566	7	CN725823 3ETMS UP
4	324.4	78.4	484	7	CN726272 3ETMS UP
5	324.4	78.4	485	7	CN726374 3ETMS UP
6	322.8	78.0	481	7	CN726255 3ETMS UP
7	320	77.3	456	7	CN726661 3ETMS UP
8	316.4	76.4	458	7	CN726701 3ETMS UP
9	315.6	76.2	597	7	CN726329 3ETMS UP
10	315.2	76.1	453	7	CN726424 3ETMS UP
11	313.8	75.8	413	7	CN826227 EL1386 Br
12	313.8	75.8	458	6	CD834994 BN45.0430
13	311.2	75.2	470	6	CD831680 BN40.060H
14	311	75.1	446	6	CD834088 BN45.040H
15	311	75.1	452	6	CD832071 BN40.0610
16	310.6	75.0	519	6	CD835064 BN45.044C
17	310	74.9	447	6	CD832592 BN40.0630
18	309.4	74.7	408	6	CD833779 BN45.0011
19	309.4	74.7	409	6	CD834090 BN45.040I
20	309.4	74.7	450	6	CD834611 BN45.042H
21	308.6	74.5	438	6	CD831294 BN40.058H
22	307	74.2	420	6	CD833944 BN45.040B

23	307	74.2	421	6	CD826491	CD826491	BN25.064A
24	307	74.2	422	6	CD833983	CD833983	BN45.040D
25	307	74.2	426	6	CD827413	CD827413	BN25.067G
26	307	74.2	438	6	CD831479	CD831479	BN40.059J
27	307	74.2	553	6	CD831014	CD831014	BN40.047K
28	305.4	73.8	418	6	CD832825	CD832825	BN40.064A
29	305.4	73.8	419	6	CD834168	CD834168	BN45.040N
30	305.4	73.8	421	6	CD833977	CD833977	BN45.040D
31	305.4	73.8	421	6	CD837517	CD837517	BN45.052I
32	303.8	73.4	453	6	CD834008	CD834008	BN45.040E
33	303.2	73.2	592	7	CN726094	CN726094	17ACDHMS
34	302.2	73.0	421	6	CD831111	CD831111	BN40.058A
35	302.2	73.0	422	6	CD831972	CD831972	BN40.061I
36	302.2	73.0	424	6	CD833048	CD833048	BN40.065M
37	302.2	73.0	480	6	CD828332	CD828332	BN25.070H
38	277.6	67.1	373	7	CN726757	CN726757	3ETMS UP
39	276	66.7	458	7	CN827136	CN827136	EL2049R Br
40	275.2	66.5	449	6	CD833047	CD833047	BN40.065M
41	268.2	64.8	425	6	CD834852	CD834852	BN45.043G
42	268.2	64.8	523	6	CD833661	CD833661	BN45.001C
43	268.2	64.8	543	6	CD828840	CD828840	BN40.040A
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45	266.6	64.4	427	6	CD833613	CD833613	BN40.067P

ALIGNMENTS

RESULT 1  
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LOCUS 3ETMS UP\_001\_G04\_10JUN2003\_010 Brassica napus 3ETMS linear EST 14-MAY-2005  
DEFINITION CDNA 5', mRNA sequence.  
ACCESSION CN726241  
VERSION CN726241.1 GI:55284043  
KEYWORDS EST.  
SOURCE Brassica napus (rape)  
ORGANISM Brassica napus  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
REFERENCE 1 (bases 1 to 484)  
Tsang,S.  
AUTHORS Gene expression in seed germination in Brassica napus  
TITLE Unpublished (2004)  
JOURNAL Contact: Ed Tsang  
COMMENT Plant Natural Products  
National Research Council of Canada  
Plant Biotechnology Institute, 110 Gymnasium Place, Saskatoon,  
Saskatchewan, S7N 0W9, Canada  
Tel: 306 975 4164  
Fax: 306 975 4839  
Email: Ed.Tsang@nrc-cnrc.gc.ca  
High quality sequence stop: 484.  
Location/Qualifiers  
1..484  
/organism="Brassica napus"  
/mol\_type="mRNA"  
/db\_xref="taxon:3708"  
/clone\_lib="Brassica napus 3ETMS"  
/note="Vector: pDNR-LIB CREATOR; Site\_1: SfiIA; Site\_2: SfiIB; Sequences have been trimmed to remove vector and low quality regions using LUCY sequence cleanup software (www.tigr.org)."

FEATURES  
source

ORIGIN

Query Match 79.1%; Score 327.6; DB 7; Length 484;  
Best Local Similarity 89.9%; Pred. No. 1e-69;  
Matches 374; Conservative 0; Mismatches 39; Indels 3; Gaps 2;  
QY 1 GTTTATTAGTCATGCGTAAAGTTTGGTCGCATCGACCTCTTTTGGCTCTTT 60  
|||||  
DB 51 GTATTACTAGTGAGCATGCGTAAAGTTTGGTCGCATCGACCTCTTTTGGCTCTTT 110  
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QY 61 GTTCTTTTTCGCTGCTTTTCGAAGCACCACCAATGGTGGAGGACAGAGTGTGCGAAGG 120  
 Db 111 GTTCTTTTTCGCTGCTTTTCGAAGCACCACCAATGGTGGAGGACAGAGTGTGCGAAGG 170  
 QY 121 CCAAGTGGGACATGGTTCAGGAGTCTGTGGAACAATAACGCATGCAAGAAATCAGTGCATT 180  
 Db 171 CCAAGTGGGACATGGTTCAGGAGTCTGTGGAACAATAACGCATGCAAGAAATCAGTGCATT 230  
 QY 181 AACCTTGAGAAAGCAGCATGATCTTGGCAACTATGTCTTCCAGCTCACAAGTGTATC 240  
 Db 231 AACCTTGAGAAAGCAGCATGATCTTGGCAACTATGTCTTCCAGCTCACAAGTGTATC 290  
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 Db 291 TGTCTACTTTCCCTGTTTAAATTTATCGCAAACTCTTTGGTGAATAGTTTATGTAATTTAC 350  
 QY 301 ACAAATAAGTCAGTGTCACTATCCATGAGTGATTTTAAAGACATGTACC--AGATATGTT 358  
 Db 351 ACAAATAAGTCAGTGTCACTATCCATGAGTGATTTTAAAGACATGTACC--AGATATGTT 410  
 QY 359 ATGTTGGTTCGGTTATACAAATAAAGTTTATTCACCAAAAAAATAAAAAA 414  
 Db 411 ATGTTGGTTCGGTTATACAAATAAAGTTTATTCACCAAAAAAATAAAAAA 465

RESULT 2  
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 LOCUS 3ETMS UP 006 C09 10JUN2003\_038 Brassica napus 3ETMS EST 14-MAY-2005  
 DEFINITION cDNA 5', mRNA sequence.  
 ACCESSION CN726625  
 VERSION CN726625.1 GI:65284427  
 KEYWORDS EST.  
 SOURCE Brassica napus (rape)  
 ORGANISM Brassica napus  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
 REFERENCE 1 (bases 1 to 547)  
 Tsang, E.  
 Gene expression in seed germination in Brassica napus  
 AUTHORS Tsang, E.  
 TITLE Unpublished (2004)  
 JOURNAL Contact: Ed Tsang  
 COMMENT Plant Natural Products  
 National Research Council of Canada  
 Plant Biotechnology Institute, 110 Gymnasium Place, Saskatoon,  
 Saskatchewan, S7N 0W9, Canada  
 Tel: 306 975 4164  
 Fax: 306 975 4839  
 Email: Ed.Tsang@nrc-cnrc.gc.ca  
 High quality sequence stop: 547.

FEATURES  
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 Location/Qualifiers  
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 /mol\_type="mRNA"  
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 /notes="Vector: pDNR-LIB CREATOR; Site 1: SfiIA; Site 2:  
 SfiIB; Sequences have been trimmed to remove vector and  
 low quality regions using LUCY sequence cleanup software  
 (www.tigr.org)."  
 ORIGIN

Query Match 78.9%; Score 326.8; DB 7; Length 547;  
 Best Local Similarity 88.2%; Pred. No. 1.6e-69;  
 Matches 367; Conservative 0; Mismatches 47; Indels 2; Gaps 1;  
 QY 1 GTTTTATTAGTATCATGGTAAAGTTTGGCTCCATCATCGCACTTCTTTTGGCTGCTCT 60  
 Db 48 GTATTACTAGTACGATGGTAAAGTTTGGCTTCCATCATGCCCCCACTTTTGGCTCTCT 107  
 QY 61 GTTCTTTTTCGCTGCTTTTCGAAGCACCACCAATGGTGGAGGACAGAGTGTGCGAAGG 120

Db 108 GTTCTTTTTCGCTGCTTTTCGAAGCACCACCAATGGTGGAGGACAGAGTGTGCGAAGG 167  
 QY 121 CCAAGTGGGACATGGTTCAGGAGTCTGTGGAACAATAACGCATGCAAGAAATCAGTGCATT 180  
 Db 168 CCAAGTGGGACATGGTTCAGGAGTCTGTGGAACAATAACGCATGCAAGAAATCAGTGCATT 227  
 QY 181 AACCTTGAGAAAGCAGCATGATCTTGGCAACTATGTCTTCCAGCTCACAAGTGTATC 240  
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 QY 241 TGTCTACTTTCCCTGTTTAAATTTATCGCAAACTCTTTGGTGAATAGTTTATGTAATTTAC 300  
 Db 288 TGTCTACTTTCCCTGTTTAAATTTATCGCAAACTCTTTGGTGAATAGTTTATGTAATTTAC 347  
 QY 301 ACAAATAAGTCAGTGTCACTATCCATGAGTGATTTTAAAGACATGTACC--AGATATGTT 358  
 Db 348 ACAAATAAGTCAGTGTCACTATCCATGAGTGATTTTAAAGACATGTACC--AGATATGTT 407  
 QY 359 ATGTTGGTTCGGTTATACAAATAAAGTTTATTCACCAAAAAAATAAAAAA 414  
 Db 408 ATGTTGGTTCGGTTATACAAATAAAGTTTATTCACCAAAAAAATAAAAAA 463

RESULT 3  
 CN725823  
 LOCUS 17ACDHMS UP 002\_F02\_28JAN2004\_006 Brassica napus 17ACDHMS Brassica  
 DEFINITION napus cDNA 5', mRNA sequence.  
 ACCESSION CN725823  
 VERSION CN725823.1 GI:65283625  
 KEYWORDS EST.  
 SOURCE Brassica napus (rape)  
 ORGANISM Brassica napus  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
 REFERENCE 1 (bases 1 to 566)  
 Fei, H., Li, F., Tsang, E. and Cutler, A.  
 Gene expression in germinating and dormant seeds of Brassica napus  
 AUTHORS Fei, H., Li, F., Tsang, E. and Cutler, A.  
 TITLE Unpublished (2004)  
 JOURNAL Contact: Adrian Cutler  
 COMMENT National Research Council of Canada  
 Plant Biotechnology Institute, 110 Gymnasium Place, Saskatoon,  
 Saskatchewan, S7N 0W9, Canada  
 Tel: 306 975 5581  
 Fax: 306 975 4839  
 Email: Adrian.Cutler@nrc-cnrc.gc.ca  
 High quality sequence stop: 566.

FEATURES  
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 /organism="Brassica napus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:3708"  
 /clone\_lib="Brassica napus 17ACDHMS"  
 /note="Vector: pDNR-LIB CREATOR; Site 1: Sfi IA; Site 2:  
 Sfi IB; Sequences have been trimmed to remove vector and  
 low quality regions using LUCY sequence cleanup software  
 (www.tigr.org)."  
 ORIGIN

Query Match 78.7%; Score 326; DB 7; Length 566;  
 Best Local Similarity 89.7%; Pred. No. 2.5e-69;  
 Matches 373; Conservative 0; Mismatches 40; Indels 3; Gaps 2;  
 QY 1 GTTTTATTAGTATCATGGTAAAGTTTGGCTCCATCATCGCACTTCTTTTGGCTGCTCT 60  
 Db 49 GTATTACTAGTACGATGGTAAAGTTTGGCTTCCATCATGCCCCCACTTTTGGCTCTCT 108  
 QY 61 GTTCTTTTTCGCTGCTTTTCGAAGCACCACCAATGGTGGAGGACAGAGTGTGCGAAGG 120  
 Db 109 GTTCTTTTTCGCTGCTTTTCGAAGCACCACCAATGGTGGAGGACAGAGTGTGCGAAGG 168

QY 121 CCAAGTGGGACATGGTCCAGGAGTCTGTGGAAACAAATAACGCATGCAAGAAATCAGTGCATT 180  
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 DB 169 CCAAGTGGGACATGGTCCAGGAGTCTGTGGAAACAAATAACGCATGCAAGAAATCAGTGCATT 228  
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 QY 181 AACCTTGAGAAAGCAGCATGGATCTTCCAACTATGCTTCCAGCTCACAAGTGATC 240  
 |||||  
 DB 229 AACCTTGAGAAAGCAGCATGGATCTTCCAACTATGCTTCCAGCTCACAAGTGATC 288  
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 QY 241 TGTACTCTTCCCTGTGTTAAATTTATCGCAAACTCTTTGGTGAATAGTTTTTATGTAATTTAC 300  
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 DB 289 TGTACTCTTCCCTGTGTTAAATTTATCGCAAACTCTTTGGTGAATAGTTTTTATGTAATTTAC 348  
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 QY 301 ACAAAATAAGTCAGTGCTACTATCCATGAGTGAATTTAAGACATGATC--AGATATGTT 358  
 |||||  
 DB 349 ATAAAAATAAGTCAGTGCTACTATCAATGAGTGAATTTATGACATGATGATGATATGTT 408  
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 QY 359 ATGTTGGTTCGGTTATACAAATAAGTTTTTATCCAAAAAATAAAAAAAAAAAAA 414  
 |||||  
 DB 409 ATGTTGGTTCGGTTATA-ATAAAAAGTTTTTATGCACCGGTAAAAAATAAAAAAAAAAAAA 463  
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RESULT 4  
 CN726272  
 LOCUS 3ETMS UP\_002\_A11\_10JUN2003\_048 Brassica napus 3ETMS Brassica napus  
 DEFINITION CDNA 5', mRNA sequence.  
 ACCESSION CN726272  
 VERSION CN726272.1 GI:65284074  
 KEYWORDS EST.  
 SOURCE Brassica napus (rape)  
 ORGANISM Brassica napus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
 1 (bases 1 to 484)  
 Tsang, E.  
 Gene expression in seed germination in Brassica napus  
 Unpublished (2004)  
 JOURNAL Contact: Ed Tsang  
 COMMENT Plant Natural Products  
 National Research Council of Canada  
 Plant Biotechnology Institute, 110 Gymnasium Place, Saskatoon,  
 Saskatchewan, S7N 0W9, Canada  
 Tel: 306 975 4164  
 Fax: 306 975 4839  
 Email: Ed.Tsang@nrc-cnrc.gc.ca  
 High quality sequence stop: 484.  
 Location/Qualifiers

FEATURES  
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 /organism="Brassica napus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:3708"  
 /clone\_lib="Brassica napus 3ETMS"  
 /note="Vector: pDNR-LIB\_CREATOR; Site\_1: SfIIA; Site\_2:  
 SfIIB; Sequences have been trimmed to remove vector and  
 low quality regions using LUCY sequence cleanup software  
 (www.tigr.org)."

ORIGIN  
 Query Match 78.4%; Score 324.4; DB 7; Length 484;  
 Best Local Similarity 89.4%; Pred. No. 6.3e-69;  
 Matches 372; Conservative 0; Mismatches 41; Indels 3; Gaps 2;

QY 1 GTTTTATTAGTATGATGCTAAGTTGGTCCATCATCGCACTCTTTTCTGCTCTT 60  
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 DB 51 GTATTACTAGTGAGCATGGCTAAGTTGCTTCATCATTTGCCCACTTTTCTGCTCTT 110  
 |||||  
 QY 61 GTTCTTTTGTGCTCTTTCGAAGCACCACAAATGGTGGAGGACAGAGTTTGGCGAAGG 120  
 |||||  
 DB 111 GTTCTTTTGTGCTCTTTCGAAGCACCACAAATGGTGGAGGACAGAGTTTGGCGAGG 170  
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 QY 121 CCAAGTGGGACATGGTCCAGGAGTCTGTGGAAACAAATAACGCATGCAAGAAATCAGTGCATT 180  
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DB 171 CCAAGTGGGACATGGTCCAGGAGTCTGTGGAAACGATAACGCATGCAAGAAATCAGTGCATT 230  
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 QY 181 AACCTTGAGAAAGCAGCATGGATCTTCCAACTATGCTTCCAGCTCACAAGTGATC 240  
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 DB 231 AACCTTGAGAAAGCAGCATGGATCTTCCAACTATGCTTCCAGCTCACAAGTGATC 290  
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 QY 241 TGTACTCTTCCCTGTGTTAAATTTATCGCAAACTCTTTGGTGAATAGTTTTTATGTAATTTAC 300  
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 DB 291 TGTACTCTTCCCTGTGTTAAATTTATCGCAAACTCTTTGGTGAATAGTTTTTATGTAATTTAC 350  
 |||||  
 QY 301 ACAAAATAAGTCAGTGCTACTATCCATGAGTGAATTTAAGACATGATC--AGATATGTT 358  
 |||||  
 DB 351 ATAAAAATAAGTCAGTGCTACTATCAATGAGTGAATTTTGTGACATGATCCTGATATGTT 410  
 |||||  
 QY 359 ATGTTGGTTCGGTTATACAAATAAGTTTTTATCCAAAAAATAAAAAAAAAAAAA 414  
 |||||  
 DB 411 ATGTTGGTTCGGTTATA-ATAAAAAGTTTTTATGCACCGGAAAAAATAAAAAAAAAAAAA 465  
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RESULT 5  
 CN726374  
 LOCUS 3ETMS UP\_003\_C06\_10JUN2003\_022 Brassica napus 3ETMS Brassica napus  
 DEFINITION CDNA 5', mRNA sequence.  
 ACCESSION CN726374  
 VERSION CN726374.1 GI:65284176  
 KEYWORDS EST.  
 SOURCE Brassica napus (rape)  
 ORGANISM Brassica napus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
 1 (bases 1 to 485)  
 Tsang, E.  
 Gene expression in seed germination in Brassica napus  
 Unpublished (2004)  
 JOURNAL Contact: Ed Tsang  
 COMMENT Plant Natural Products  
 National Research Council of Canada  
 Plant Biotechnology Institute, 110 Gymnasium Place, Saskatoon,  
 Saskatchewan, S7N 0W9, Canada  
 Tel: 306 975 4164  
 Fax: 306 975 4839  
 Email: Ed.Tsang@nrc-cnrc.gc.ca  
 High quality sequence stop: 485.  
 Location/Qualifiers

FEATURES  
 source  
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 /organism="Brassica napus"  
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 /db\_xref="taxon:3708"  
 /clone\_lib="Brassica napus 3ETMS"  
 /note="Vector: pDNR-LIB\_CREATOR; Site\_1: SfIIA; Site\_2:  
 SfIIB; Sequences have been trimmed to remove vector and  
 low quality regions using LUCY sequence cleanup software  
 (www.tigr.org)."

ORIGIN  
 Query Match 78.4%; Score 324.4; DB 7; Length 485;  
 Best Local Similarity 89.4%; Pred. No. 6.3e-69;  
 Matches 372; Conservative 0; Mismatches 41; Indels 3; Gaps 2;

QY 1 GTTTTATTAGTATGATGCTAAGTTGGTCCATCATCGCACTCTTTTCTGCTCTT 60  
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 DB 52 GTATTACTAGTGAGCATGGCTAAGTTGCTTCATCATTTGCCCACTTTTCTGCTCTC 111  
 |||||  
 QY 61 GTTCTTTTGTGCTCTTTCGAAGCACCACAAATGGTGGAGGACAGAGTTTGGCGAAGG 120  
 |||||  
 DB 112 GTTCTTTTGTGCTCTTTCGAAGCACCACAAATGGTGGAGGACAGAGTTTGGCGAGG 171  
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 QY 121 CCAAGTGGGACATGGTCCAGGAGTCTGTGGAAACAAATAACGCATGCAAGAAATCAGTGCATT 180  
 |||||  
 DB 172 CCAAGTGGGACATGGTCCAGGAGTCTGTGGAAACAAATAACGCATGCAAGAAATCAGTGCATT 231  
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QY 181 AACCTTGAGAAAGCAGCATGATCTTGCACATATGCTCTCCAGCTCACAAAGTGATC 240  
 Db 232 AACCTTGAGAAAGCAGCATGATCTTGCACATATGCTCTCCAGCTCACAAAGTGATC 291  
 QY 241 TGTACTTTCCTTGTAAATTTATCGAAACTCTTTGGTGAATAGTTTATGTAATTTAC 300  
 Db 292 TGTACTTTCCTTGTAACTCATCGCAACTCTTTGGTGGTGTAGTTTGTGTAATTTAC 351  
 QY 301 ACAAAATAAGTCAGTGTCACTATCCAGTAGTGAATTTAAGACATGTACC--AGATATGTT 358  
 Db 352 ATAAATAAGTCGTGTCACTATCAATGAGTGATTTATGACATGTACCTGATATATGTT 411  
 QY 359 ATGTTGGTTCGGTTATACAAATAAAGTTTATTCACCAAAAAAATAAAAAA 414  
 Db 412 ATGTTGGTTCGGTTATA-ATAAAAAGTTTATGACCAATAAAAAAATAAAAAA 466

RESULT 6  
 LOCUS CN726255 481 bp mRNA linear EST 14-MAY-2005  
 DEFINITION 3ETMS UP\_001\_H06\_10JUN2003\_017 Brassica napus 3ETMS Brassica napus  
 cDNA 5', mRNA sequence.  
 ACCESSION CN726255  
 VERSION CN726255.1 GI:65284057  
 KEYWORDS EST.  
 SOURCE Brassica napus (rape)  
 ORGANISM Brassica napus  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
 REFERENCE 1 (bases 1 to 481)  
 AUTHORS Tsang,E.  
 TITLE Gene expression in seed germination in Brassica napus  
 JOURNAL Unpublished (2004)  
 COMMENT Contact: Ed Tsang  
 Plant Natural Products  
 National Research Council of Canada  
 Plant Biotechnology Institute, 110 Gymnasium Place, Saskatoon,  
 Saskatchewan, S7N 0W9, Canada  
 Tel: 306 975 4164  
 Fax: 306 975 4839  
 Email: Ed.Tsang@nrc-cnrc.gc.ca  
 High quality sequence stop: 481.

FEATURES  
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 /organism="Brassica napus"  
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 /db\_xref="taxon:3708"  
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 /note="Vector: pDNR-LIB\_CREATOR; Site\_1: SfIIA; Site\_2:  
 SfIIB; Sequences have been trimmed to remove vector and  
 low quality regions using LUCY sequence cleanup software  
 (www.tigr.org)."  
 ORIGIN

Query Match 78.0%; Score 322.8; DB 7; Length 481;  
 Best Local Similarity 89.2%; Pred. No. 1.5e-68;  
 Matches 371; Conservative 0; Mismatches 42; Indels 3; Gaps 2;  
 QY 1 GTTTTATTAGTATCATGGCTAAGTTTGGCTCATCATCGCACTCTCTTTTGGCTGCTCT 60  
 Db 51 GTATTACTAGTACGCGCTAAGTTTGGCTTCCATCATTTGCCCACTTTTGGCTGCTCT 110  
 QY 61 GTTCTTTTGTCTCTTTCGAAGCACCACCAATCGTGGAGACACAGAAGTTGTGCGAAAGG 120  
 Db 111 GTTCTTTTGTCTCTTTCGAAGCACCACCAATCGTGGAGACACAGAAGTTGTGCGAGAG 170  
 QY 121 CCAAGTGGGACATGGTTCAGAGTCTGTGGAAACAATAACCATGCAAGATCAGTGCATT 180  
 Db 171 CCAAGTGGGACATGGTTCAGAGTCTGTGGAAACAATAACCATGCAAGATCAGTGCATT 230  
 QY 181 AACCTTGAGAAAGCAGCATGATCTTGCACATATGCTCTTCCAGCTCACAAAGTGATC 240

Db 231 AACCTTGAGAAAGCAGCATGATCTTGCACATATGCTCTTCCAGCTCACAAAGTGATC 290  
 QY 241 TGTACTTTCCTTGTAAATTTATCGAAACTCTTTGGTGAATAGTTTATGTAATTTAC 300  
 Db 291 TGTACTTTCCTTGTAACTCATCGCAACTCTTTGGTGGTGTAGTTTGTGTAATTTAC 350  
 QY 301 ACAAAATAAGTCAGTGTCACTATCCAGTAGTGAATTTAAGACATGTACC--AGATATGTT 358  
 Db 351 ATAAATAAGTCGTGTCACTATCAATGAGTGATTTATGACATGTACCTGATATATGTT 410  
 QY 359 ATGTTGGTTCGGTTATACAAATAAAGTTTATTCACCAAAAAAATAAAAAA 414  
 Db 411 ATGTTGGTTCGGTTATA-ATAAAAAGTTTATGCGCAAAAAAATAAAAAA 465

RESULT 7  
 LOCUS CN726661 456 bp mRNA linear EST 14-MAY-2005  
 DEFINITION 3ETMS UP\_006\_G02\_10JUN2003\_002 Brassica napus 3ETMS Brassica napus  
 cDNA 5', mRNA sequence.  
 ACCESSION CN726661  
 VERSION CN726661.1 GI:65284463  
 KEYWORDS EST.  
 SOURCE Brassica napus (rape)  
 ORGANISM Brassica napus  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
 REFERENCE 1 (bases 1 to 456)  
 AUTHORS Tsang,E.  
 TITLE Gene expression in seed germination in Brassica napus  
 JOURNAL Unpublished (2004)  
 COMMENT Contact: Ed Tsang  
 Plant Natural Products  
 National Research Council of Canada  
 Plant Biotechnology Institute, 110 Gymnasium Place, Saskatoon,  
 Saskatchewan, S7N 0W9, Canada  
 Tel: 306 975 4164  
 Fax: 306 975 4839  
 Email: Ed.Tsang@nrc-cnrc.gc.ca  
 High quality sequence stop: 456.

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 /organism="Brassica napus"  
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 /db\_xref="taxon:3708"  
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 SfIIB; Sequences have been trimmed to remove vector and  
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 (www.tigr.org)."  
 ORIGIN

Query Match 77.3%; Score 320; DB 7; Length 456;  
 Best Local Similarity 87.9%; Pred. No. 7.5e-68;  
 Matches 364; Conservative 0; Mismatches 40; Indels 10; Gaps 1;  
 QY 1 GTTTTATTAGTATCATGGCTAAGTTTGGCTCATCATCGCACTCTCTTTTGGCTGCTCT 60  
 Db 36 GTATTACTAGTATCATGGCTAAGTTTGGCTTCCATCATTTGCCCTACTTTTGGCTGCTCT 95  
 QY 61 GTTCTTTTGTCTCTTTCGAAGCACCACCAATCGTGGAGACACAGAAGTTGTGCGAAAGG 120  
 Db 96 GTCTTTTTCGTCTCTTTCGAAGCACCACCAATCGTGGAGACACAGAAGTTGTGCGAGAG 155  
 QY 121 CCAAGTGGGACATGGTTCAGAGTCTGTGGAAACAATAACCATGCAAGATCAGTGCATT 180  
 Db 156 CCAAGTGGGACATGGTTCAGAGTCTGTGGAAACAATAACCATGCAAGATCAGTGCATT 215  
 QY 181 AACCTTGAGAAAGCAGCATGATCTTGCACATATGCTCTTCCAGCTCACAAAGTGATC 240  
 Db 216 AACCTTGAGAAAGCAGCATGATCTTGCACATATGCTCTTCCAGCTCACAAAGTGATC 275

QY 241 TGCTACTTTCCTGTGTAATTAATCGCAAACTCTTTGGTGAATAGTTTTTATGTAATTTAC 300  
 DB 276 TGCTACTTCCCTGTGTAATTAATCGCAAACTCTTTGGTGAATAGTTTTTATGTAATTTAC 335  
 QY 301 ACAAAATAGTCAGTGTCACTATCCATGAGTGAATTTTAAGACATGTACCAGATATGTTAT 360  
 DB 336 ATAAATAAGTCTGTGTCACTATCAATGATGATTTTATGACATGTACCTGATATGTTAT 395  
 QY 361 GTTGGTTCGGTTATACAAATAAAGTTTTTATTCACCAAAAAAATAAAAAA 414  
 DB 396 GTTATAATATAAAGTTTTTATGCACCTCGAAAAAATAAAAAA 449  
 DB 396 GTT-----ATATATAAAGTTTTTATGCACCAAAAAAATAAAAAA 439

RESULT 8  
 CN726701  
 LOCUS  
 DEFINITION 3ETMS UP 007 B11.11JUN2003\_047 Brassica napus 3ETMS Brassica napus  
 CDNA 5', mRNA sequence.  
 ACCESSION CN726701  
 VERSION CN726701.1 GI:65284503  
 KEYWORDS EST.  
 SOURCE Brassica napus (rape)  
 ORGANISM Brassica napus  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
 REFERENCE 1 (bases 1 to 458)  
 AUTHORS Tsang,E.  
 TITLE Gene expression in seed germination in Brassica napus  
 JOURNAL Unpublished (2004)  
 COMMENT Contact: Ed Tsang  
 Plant Natural Products  
 National Research Council of Canada  
 Plant Biotechnology Institute, 110 Gymnasium Place, Saskatoon,  
 Saskatchewan, S7N 0W9, Canada  
 Tel: 306 975 4164  
 Fax: 306 975 4839  
 Email: Ed.Tsang@nrc-cnrc.gc.ca  
 High quality sequence stop: 458.

## FEATURES

source  
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 /organism="Brassica napus"  
 /mol\_type="mRNA"  
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 /clone\_lib="Brassica napus 3ETMS"  
 /note="Vector: pDNR-LIB\_CREATOR; Site\_1: SfiIA; Site\_2:  
 SfiIB; Sequences have been trimmed to remove vector and  
 low quality regions using LUCY sequence cleanup software  
 (www.tigr.org)."  
 ORIGIN

Query Match 76.4%; Score 316.4; DB 7; Length 458;  
 Best Local Similarity 85.3%; Pred. No. 5.7e-87;  
 Matches 353; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 1 GTTTATTAGTATCATGGCTAAGTTTGGTCCATCATCGCACTCTTTTGTGCTCTT 60  
 DB 36 GTATTACTAGTATCATGGCTAAGTTTGGTCCATCATCGCACTCTTTTGTGCTCTT 95  
 QY 61 GTTCTTTTGTGCTCTTTCGAAGCACCAACAATGGTGGAAAGCACAGAGTTGTGCGAAAGG 120  
 DB 96 GTCCTTTTGTGCTCTTTCGAAGCACCAACAATGGTGGAAAGCACAGAGTTGTGCGAGAGG 155  
 QY 121 CCAAGTGGGACATGGTCAGAGTCTGTGGAAACAATAACGCATGCAAGATCAGTGCATT 180  
 DB 156 CCAAGTGGGACATGGTCAGAGTCTGTGGAAACAATAACGCATGCAAGATCAGTGCATT 215  
 QY 181 AACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCAGCTCACAGTGTATC 240  
 DB 216 AACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCAGCTCACAGTGTAT 275  
 QY 241 TGCTACTTTCCTGTGTAATTAATCGCAAACTCTTTGGTGAATAGTTTTTATGTAATTTAC 300

DB 276 TGCTACTTCCCTGTGTAATTAATCGCAAACTCTTTGGTGAATAGTTTTTATGTAATTTAC 335  
 QY 301 ACAAAATAGTCAGTGTCACTATCCATGAGTGAATTTTAAGACATGTACCAGATATGTTAT 360  
 DB 336 ATAAATAAGTCTGTGTCACTATCAATGATGATTTTATGACATGTACCTGATATGTTAT 395  
 QY 361 GTTGGTTCGGTTATACAAATAAAGTTTTTATTCACCAAAAAAATAAAAAA 414  
 DB 396 GTTATAATATAAAGTTTTTATGCACCTCGAAAAAATAAAAAA 449

## RESULT 9

CN726329  
 LOCUS  
 DEFINITION 3ETMS UP\_002 G01.10JUN2003\_002 Brassica napus 3ETMS Brassica napus  
 CDNA 5', mRNA sequence.  
 ACCESSION CN726329  
 VERSION CN726329.1 GI:65284131  
 KEYWORDS EST.  
 SOURCE Brassica napus (rape)  
 ORGANISM Brassica napus  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
 REFERENCE 1 (bases 1 to 597)  
 AUTHORS Tsang,E.  
 TITLE Gene expression in seed germination in Brassica napus  
 JOURNAL Unpublished (2004)  
 COMMENT Contact: Ed Tsang  
 Plant Natural Products  
 National Research Council of Canada  
 Plant Biotechnology Institute, 110 Gymnasium Place, Saskatoon,  
 Saskatchewan, S7N 0W9, Canada  
 Tel: 306 975 4164  
 Fax: 306 975 4839  
 Email: Ed.Tsang@nrc-cnrc.gc.ca  
 High quality sequence stop: 597.

## FEATURES

source  
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 Location/Qualifiers  
 /organism="Brassica napus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:3708"  
 /clone\_lib="Brassica napus 3ETMS"  
 /note="Vector: pDNR-LIB\_CREATOR; Site\_1: SfiIA; Site\_2:  
 SfiIB; Sequences have been trimmed to remove vector and  
 low quality regions using LUCY sequence cleanup software  
 (www.tigr.org)."  
 ORIGIN

Query Match 76.2%; Score 315.6; DB 7; Length 597;  
 Best Local Similarity 88.6%; Pred. No. 9.1e-67;  
 Matches 365; Conservative 0; Mismatches 44; Indels 3; Gaps 2;

QY 1 GTTTATTAGTATCATGGCTAAGTTTGGTCCATCATCGCACTCTTTTGTGCTCTT 60  
 DB 51 GTATTACTAGTATGAGCATGGCTAAGTTTGGTCTTCATCATTTGCCCACTCTTTTGTGCTCTT 110  
 QY 61 GTTCTTTTGTGCTCTTTCGAAGCACCAACAATGGTGGAAAGCACAGAGTTGTGCGAAAGG 120  
 DB 111 GTTCTTTTGTGCTCTTTCGAAGCACCAACAATGGTGGAAAGCACAGAGTTGTGCGAGAGG 170  
 QY 121 CCAAGTGGGACATGGTCAGAGTCTGTGGAAACAATAACGCATGCAAGATCAGTGCATT 180  
 DB 171 CCAAGTGGGACATGGTCAGAGTCTGTGGAAACAATAACGCATGCAAGATCAGTGCATT 230  
 QY 181 AACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCAGCTCACAGTGTATC 240  
 DB 231 AACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCAGCTCACAGTGTAT 290  
 QY 241 TGCTACTTTCCTGTGTAATTAATCGCAAACTCTTTGGTGAATAGTTTTTATGTAATTTAC 300  
 DB 291 TGCTACTTCCCTGTGTAATTAATCGCAAACTCTTTGGTGAATAGTTTTTATGTAATTTAC 350

```

QY 301 ACAATAAAGTCAGTGTCTACTATCCATGAGTGATTTTAAGACATGTACC--AGATATGTT 358
Db 351 ATAAATAAAGTCGTGTCTACTATCAATGAGTGATTTATGACATGACCTGATATGTT 410
QY 359 ATGTTCGGTTCGGTTATACAAATAAAGTTTATTACCAAAAAAATAAAAAA 410
Db 411 ATGTTCGGTTCGGTTATA-ATAAAGTTTATGACCCGTAAATAGNATATA 461

RESULT 10
LOCUS CN726424
DEFINITION 3ETMS UP_003_H02_10JUN2003_001 Brassica napus 3ETMS Brassica napus
ACCESSION CDNA 5', mRNA sequence.
VERSION CN726424
KEYWORDS CN726424.1 GI:65284226
SOURCE EST.
ORGANISM Brassica napus (rape)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 453)
AUTHORS Tsang,E.
TITLE Gene expression in seed germination in Brassica napus
JOURNAL Unpublished (2004)
COMMENT Contact: Ed Tsang
Plant Natural Products
National Research Council of Canada
Plant Biotechnology Institute, 110 Gymnasium Place, Saskatoon,
Saskatchewan, S7N 0W9, Canada
Tel: 306 975 4164
Fax: 306 975 4839
Email: Ed.Tsang@nrc-cnrc.gc.ca
High quality sequence stop: 453.

FEATURES
source
1..453
Location/Qualifiers
/organism="Brassica napus"
/mol_type="mRNA"
/db_xref="taxon:3708"
/clone_lib="Brassica napus 3ETMS"
/notes="Vector: pDNR-LIB CREATOR; Site 1: SfIIA; Site 2:
SfiIB; Sequences have been trimmed to remove vector and
low quality regions using LUCY sequence cleanup software
(www.tigr.org)."

ORIGIN
Query Match 76.1%; Score 315.2; DB 7; Length 453;
Best Local Similarity 87.2%; Pred. No. 1.1e-66;
Matches 361; Conservative 0; Mismatches 43; Indels 10; Gaps 1;

QY 1 GTTTTATTAGTGATCGCTAAGTTTGGTTCATCATCGCACTCTTTTGTGCTCTT 60
Db 36 GTATTACTAGTGATCATGCTAAGTTTGTCTCCATCATTTGCCCTACTTTTGTGCTCTT 95
QY 61 GTTCTTTTGTGCTTTTGAAGCACCACCAATGGTGGAGACACAGAGTTGTGCGAAGG 120
Db 96 GTCTTTTGTGCTCTCTCGAAGCACCACCAATGGTGGAGACACAGAGTTGTGCGAAGG 155
QY 121 CCAAGTGGGACATGGTCAGAGTCTGTGGAACAATAACGCATGCAAGAAATCAGTGCATT 180
Db 156 CCAAGTGGGACATGGTCAGAGTCTGTGGAACAATAACGCATGCAAGAAATCAGTGCATT 215
QY 181 AACCTTTGAGAAAGCAGACATGGATCTTGCAACTATGTCTTCCAGCTCACAGTGTATC 240
Db 216 AACCTTTGAGAAAGCAGACATGGATCTTGCAACTATGTCTTCCAGCTCACAGTGTATC 275
QY 241 TGTACTTTCTTTGTTAAATTTATCGCAAACTCTTTGGTGAATAGTTTTATGTAATTTAC 300
Db 276 TGTACTTCCCTTTGTTAACTTATGCGCAAACTCTATGTTGGTGGTTAGTTTGTGTAATTTAC 335
QY 301 ACAATAAAGTCAGTGTCTACTATCCATGAGTGATTTTAAGACATGTACCAGATATGTTAT 360

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Db 336 ATAAATAAAGTCGTGTCTACTATCAATGAGTGATTTATGACATGTACCTGATATGTTAT 395
QY 361 GTTGTTCGGTTATACAAATAAAGTTTATTACCAAAAAAATAAAAAA 414
Db 396 GTT-----ATAATATAAAGTTTATATACAAAAAATAAAAAA 439

RESULT 11
LOCUS CN826227
DEFINITION 413 bp mRNA linear EST 14-MAY-2005
ACCESSION EL1386 Brassica embryo library (EL) Brassica napus cDNA clone
VERSION EL1386 complete, mRNA sequence.
KEYWORDS CN826227.1 GI:65296011
SOURCE EST.
ORGANISM Brassica napus (rape)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 413)
AUTHORS Sharpe,A.G., Gjetvaj,B., Durkin,J. and Lydiate,D.J.
TITLE Brassica napus ESTs
JOURNAL Unpublished (2004)
COMMENT Contact: Sharpe, A.G.
Molecular Genetics
Agriculture & Agri-Food Canada
107 Science Place, Saskatoon, Saskatchewan, Canada, S7N0X2
Tel: 306 956 7271
Fax: 306 956 7247
Email: sharpea@agr.gc.ca
Seq primer: M13 Forward and T7.
Location/Qualifiers
1..413
/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="DH12075 (double haploid line from Cresor x
Westar cross)"
/db_xref="taxon:3708"
/clone_lib="EL1386"
/db_xref="EL1386"
/dev_stage="Mid to late embryos (4-6 mg)"
/lab_host="E. coli Electromax DH5 alpha-e"
/clone_lib="Brassica embryo library (EL)"
/notes="Organ: Embryos without seed coat; Vector: pSPORT1
(modified: GCGCCGCC*GACTAGTGCCTC*cgagcgcgggtcgac);
Site 1: NotI; Site 2: SalI; Seeds were collected by Dr.
Francois Ouellet when they were still very green (mid to
large stage, cotyledons were formed). The seed coats were
removed and the remaining tissue was used for cDNA library
construction. mRNA was poly-A primed using SuperScript
Plasmid System cDNA Synthesis and Cloning kit (Invitrogen)
After initial screening, the most abundant redundant
clones were screened out using 22 oligos designed to match
napins (including albumins), cruciferins, oleosins,
trypsin inhibitor 2, cytosolic GAPDH, cyclophilins, HSP70,
desaturase, and CAB (LHCP)."

ORIGIN
Query Match 75.8%; Score 313.8; DB 7; Length 413;
Best Local Similarity 87.3%; Pred. No. 2.5e-66;
Matches 359; Conservative 0; Mismatches 42; Indels 10; Gaps 1;

QY 1 GTTTTATTAGTGATCATGCTAAGTTTGGTTCATCATCGCACTCTTTTGTGCTCTT 60
Db 13 GTATTACTAGTGATCATGCTAAGTTTGTCTTCATCATTTGCCCTACTTTTGTGCTCTT 72
QY 61 GTTCTTTTGTGCTTTTGAAGCACCACCAATGGTGGAGACACAGAGTTGTGCGAAGG 120
Db 73 GTCTTTTGTGCTCTCTCGAAGCACCACCAATGGTGGAGACACAGAGTTGTGCGAAGG 132
QY 121 CCAAGTGGGACATGGTTCAGGAGTCTGTGGAACAATAACGCATGCAAGAAATCAGTGCATT 180

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Db 133 CCAAGTGGGACATGGTCAAGAGTCTGTGGAACAATAACGCATGCAAGAAATCAGTGCATT 192

QY 181 AACCTTTGAGAAAGCAGACATGGATCTTGCAACTATGTCTTCCAGCTCACAAGTGTATC 240

Db 193 AACCTTGAGAAAGCAGACATGGATCTTGCAACTATGTCTTCCAGCTCACAAGTGTAT 252

QY 241 TGTCTACTTCCCTTGTGTTAAATTAATGCGCAAACTCTTTGGTGGTGAATGTTTATGTAATTTAC 300

Db 253 TGTCTACTTCCCTTGTGTTAACTTATGCGCAAACTCTTTGGTGGTGAATGTTTATGTAATTTAC 312

QY 301 ACAAAATAAGTCAGTCTCACTATCCATGATGATTTTAAGACATGATGATGATGATGATGAT 360

Db 313 ATAAATAAGTCAGTCTCACTATCCATGATGATTTTAAGACATGATGATGATGATGATGAT 372

QY 361 GTTGGTTCGGTTATACAAATAAGTTTTATTCACCAAAAAAATTTTATTTTATTTTATTTTAT 411

Db 373 GTT-----ATAATATAAGTTTTATTCACCAAAAAAATTTTATTTTATTTTATTTTATTTTAT 413

RESULT 12  
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LOCUS  
DEFINITION BN45\_043006F011229 BN45 Brassica napus cDNA clone BN45043006, mRNA  
ACCESSION CD834994  
VERSION CD834994.1 GI:32516934  
KEYWORDS  
SOURCE Brassica napus (rape)  
ORGANISM Brassica napus  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
REFERENCE 1 (bases 1 to 458)  
AUTHORS  
TITLE Genoplatte, a major partnership french program in plant genomics  
JOURNAL Unpublished (2003)  
COMMENT Contact: Genoplatte  
93, rue Henri Rochefort 91025 EVRY CEDEX France  
Tel: 33 1 69 47 54 00  
Fax: 33 1 69 47 54 10  
This sequence has been generated in the framework of the french  
plant genomics programme 'Genoplatte' (<http://www.genoplatte.com>  
and <http://genoplatte-info.infobiogen.fr>).

FEATURES  
source  
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/organism="Brassica napus"  
/mol\_type="mRNA"  
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/db\_xref="taxon:3708"  
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/clone\_lib="BN45"

ORIGIN  
Query Match 75.8%; Score 313.8; DB 6; Length 458;  
Best Local Similarity 88.7%; Pred. No. 2.5e-66;  
Matches 362; Conservative 0; Mismatches 43; Indels 3; Gaps 2;

QY 1 GTTTTATTAGTATGATGCTAAGTTTGGTGCATCATCGCACTCTTTTTCGCTCTTT 60

Db 51 GTATTACTAGTGAGCATGGCTAAGTTTGGTTCATCATTCGCCCACTTTTTCGCTCTTT 110

QY 61 GTTCTTTTTCGCTCTTCCAGCACCAACAATGGTGGAGGACAGAGTTGTCGCAAGG 120

Db 111 GTTCTTTTTCGCTCTTCCAGCACCAACAATGGTGGAGGACAGAGTTGTCGCAAGG 170

QY 121 CCAAGTGGACATGGTCAGAGTCTGTGGAACAATAACGCATGCAAGAAATCAGTGCATT 180

Db 171 CCAAGTGGACATGGTCAGAGTCTGTGGAACAATAACGCATGCAAGAAATCAGTGCATT 230

QY 181 AACCTTGAGAAAGCAGACATGGATCTTGCAACTATGTCTTCCAGCTCACAAGTGTATC 240

Db 231 AACCTTGAGAAAGCAGACATGGATCTTGCAACTATGTCTTCCAGCTCACAAGTGTATT 290

QY 241 TGTCTACTTTCCTTGTGTTAAATTTATCGCAAACTCTTTGGTGAATGTTTATGTAATTTAC 300

Db 291 TGTCTACTTTCCTTGTGTTAACTTATGCGCAAACTCTTTGGTGGTGAATGTTTATGTAATTTAC 350

QY 301 ACAAAATAAGTCAGTCTCACTATCCATGATGATTTTAAGACATGATGATGATGATGATGAT 358

Db 351 ATAAATAAGTCAGTCTCACTATCCATGATGATTTTAAGACATGATGATGATGATGATGAT 410

QY 359 ATGTTGGTTCGGTTATACAAATAAGTTTTATTCACCAAAAAAATTTTATTTTATTTTATTTTAT 406

Db 411 ATGTTGGTTCGGTTATATA-ATAAAAGTTTTATGACCCCGTANAATAGAA 457

RESULT 13  
CD831680  
LOCUS  
DEFINITION BN40\_060H13F011227 BN40 Brassica napus cDNA clone BN40060H13, mRNA  
ACCESSION CD831680  
VERSION CD831680.1 GI:32513620  
KEYWORDS  
SOURCE EST.  
ORGANISM Brassica napus (rape)  
Brassica napus  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
REFERENCE 1 (bases 1 to 470)  
AUTHORS  
TITLE Genoplatte, a major partnership french program in plant genomics  
JOURNAL Unpublished (2003)  
COMMENT Contact: Genoplatte  
93, rue Henri Rochefort 91025 EVRY CEDEX France  
Tel: 33 1 69 47 54 00  
Fax: 33 1 69 47 54 10  
This sequence has been generated in the framework of the french  
plant genomics programme 'Genoplatte' (<http://www.genoplatte.com>  
and <http://genoplatte-info.infobiogen.fr>).

FEATURES  
source  
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/organism="Brassica napus"  
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/clone="BN40060H13"  
/tissue\_type="seed"  
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ORIGIN  
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Best Local Similarity 89.7%; Pred. No. 1.1e-65;  
Matches 357; Conservative 0; Mismatches 38; Indels 3; Gaps 2;

QY 1 GTTTTATTAGTATGATCATGGCTAAGTTTGGTGCATCATCGCACTTCTTTTTCGCTCTTT 60

Db 73 GTATTACTAGTGAGCATGGCTAAGTTTGGTTCATCATTCGCCCACTTTTTCGCTCTTT 132

QY 61 GTTCTTTTTCGCTCTTTCGAAGCACCAACAATGGTGGAGGACAGAGTTGTCGCAAGG 120

Db 133 GTTCTTTTTCGCTCTTTCGAAGCACCAACAATGGTGGAGGACAGAGTTGTCGCAAGG 192

QY 121 CCAAGTGGACATGGTCAGAGTCTGTGGAACAATAACGCATGCAAGAAATCAGTGCATT 180

Db 193 CCAAGTGGACATGGTCAGAGTCTGTGGAACAATAACGCATGCAAGAAATCAGTGCATT 252

QY 181 AACCTTGAGAAAGCAGACATGGATCTTGCAACTATGTCTTCCAGCTCACAAGTGTATC 240

Db 253 AACCTTGAGAAAGCAGACATGGATCTTGCAACTATGTCTTCCAGCTCACAAGTGTATT 312

QY 241 TGTCTACTTTCCTTGTGTTAAATTTATCGCAAACTCTTTGGTGAATGTTTATGTAATTTAC 300

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Db 313 TGCTACTCCCTGGTTAACTTATGCGCAAACTCTTTGGTGGTTAGTTTGTGTAAATTTAC 372
QY 301 ACAAAATAGTCAGTCTCACTATCCATGAGTGAATTTTAAGACATGTACC--AGATATGTT 358
Db 373 ATAAATATAGTCTGTCTCACTATCAATGAGTGAATTTATGACATGTACCTGATATATGTT 432
QY 359 ATGTTGGTTCGGTTATACAAATAAAGTTTATTCACCA 396
Db 433 ATGTTGGTTCGGTTATA-ATAAAAGTTTATGCACCA 469

RESULT 14
CD834068
LOCUS DEFINITION
CD834068 446 bp mRNA linear EST 10-JUL-2003
CD834068.1 GI:32516008
Brassica napus (rape)
Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 446)
Genoplante.
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Genoplante, a major partnership french program in plant genomics
Unpublished (2003)
Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).
FEATURES
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Location/Qualifiers
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/cultivar="Jet Neuf"
/db_xref="taxon:3708"
/clone="BN45040H17"
/tissue_type="seed"
/clone_lib="BN45"

ORIGIN
Query Match 75.1%; Score 311; DB 6; Length 446;
Best Local Similarity 89.2%; Pred. No. 1.2e-65;
Matches 347; Conservative 0; Mismatches 40; Indels 2; Gaps 1;

QY 1 GTTTTATTAGTATCATGGCTAAGTTTGGTCCATCATCGCACTCTTTTGTGCTCTTT 60
Db 51 GTATTACTAGTGAGCATGGCTAAGTTTGGTTCATCATTTGCCCACTTTTGTGCTCTT 110
QY 61 GTTCTTTTGTCTCTTTCGAAGCACCAACAATGGTGGAGCACAGAAAGTTTGCGAAGG 120
Db 111 GTTCTTTTGTCTCTTTCGAAGCACCAACAATGGTGGAGCACAGAAAGTTTGCGAGAG 170
QY 121 CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATT 180
Db 171 CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATT 230
QY 181 AACCTTGAGNAAGCAGACATGATCTTGCACATATGTCTTCCAGCTCACAAGTGTATC 240
Db 231 AACCTTGAGNAAGCAGACATGATCTTGCACATATGTCTTCCAGCTCACAAGTGTAT 290
QY 241 TGTCTCTTCTTGTGTTAAATTTATCGCAAACTCTTTGGTGAATGTTTATGTAATTTAC 300
Db 291 TGTCTCTTCTTGTGTTAACTTATGCGCAAACTCTTTGGTGGTGGTGGTGGTGGTGGTGG 350
QY 301 ACAAAATAGTCAGTCTCACTATCCATGAGTGAATTTTAAGACATGTACC--AGATATGTT 358
Db 358 ATAAATATAGTCTGTCTCACTATCAATGAGTGAATTTATGACATGTACCTGATATATGTT 414
QY 359 ATGTTGGTTCGGTTATACAAATAAAGTTT 387
Db 387 ATGTTGGTTCGGTTATACAAATAAAGTTT 414
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Db 351 ATAAATAAGTCTGTGTCACTATCAATGAGTGAATTTTATGACATGTACCTGATATATGTT 410
QY 359 ATGTTGGTTCGGTTATACAAATAAAGTTT 387
Db 411 ATGTTGGTTCGGTTATATAAATAAAGTTT 439

RESULT 15
CD832071
LOCUS DEFINITION
CD832071 452 bp mRNA linear EST 10-JUL-2003
CD832071.1 GI:32514011
Brassica napus (rape)
Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 452)
Genoplante.
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Genoplante, a major partnership french program in plant genomics
Unpublished (2003)
Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).
FEATURES
source
1..452
Location/Qualifiers
/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jet Neuf"
/db_xref="taxon:3708"
/clone="BN40061003"
/tissue_type="seed"
/clone_lib="BN40"

ORIGIN
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Best Local Similarity 89.2%; Pred. No. 1.2e-65;
Matches 347; Conservative 0; Mismatches 40; Indels 2; Gaps 1;

QY 1 GTTTTATTAGTATCATGGCTAAGTTTGGTCCATCATCGCACTCTTTTGTGCTCTTT 60
Db 55 GTATTACTAGTGAGCATGGCTAAGTTTGGTTCATCATTTGCCCACTTTTGTGCTCTTT 114
QY 61 GTTCTTTTGTCTCTTTCGAAGCACCAACAATGGTGGAGCACAGAAAGTTTGCGAAGG 120
Db 115 GTTCTTTTGTCTCTTTCGAAGCACCAACAATGGTGGAGCACAGAAAGTTTGCGAGAG 174
QY 121 CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATT 180
Db 175 CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATT 234
QY 181 AACCTTGAGAAAGCAGACATGATCTTGCACATATGTCTTCCAGCTCACAAGTGTATC 240
Db 235 AACCTTGAGAAAGCAGACATGATCTTGCACATATGTCTTCCAGCTCACAAGTGTAT 294
QY 241 TGTCTCTTCTTGTGTTAAATTTATCGCAAACTCTTTGGTGAATGTTTATGTAATTTAC 300
Db 295 TGTCTCTTCTTGTGTTAACTTATGCGCAAACTCTTTGGTGGTGGTGGTGGTGGTGGTGG 354
QY 301 ACAAAATAGTCAGTCTCACTATCCATGAGTGAATTTTAAGACATGTACC--AGATATGTT 358
Db 355 ATAAATATAGTCTGTCTCACTATCAATGAGTGAATTTATGACATGTACCTGATATATGTT 414
QY 359 ATGTTGGTTCGGTTATACAAATAAAGTTT 387
Db 387 ATGTTGGTTCGGTTATACAAATAAAGTTT 414
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Db 415 ATGTTGGTTCGGTTATAATAAAAAAGTTTT 443

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Job time : 3758 secs

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GenCore version 5.1.1.8  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - nucleic search using frame\_plus.p2n model

Run on: May 10, 2006, 05:46:44 ; Search time 3626 Seconds  
(without alignments)  
1881.195 Million cell updates/sec

Title: US-09-759-584-59

Perfect score: 441

Sequence: 1 MAKFASIIALLFAALVLFPA.....RHGSCNYVPPAHKICYPFC 80

Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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3: gb.env.\*  
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5: gb.ov.\*  
6: gb.pat.\*  
7: gb.ph.\*  
8: gb.pr.\*  
9: gb.ro.\*  
10: gb.sts.\*  
11: gb.ev.\*  
12: gb.un.\*  
13: gb.vi.\*  
14: gb.hcg.\*  
15: gb.pl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	441	100.0	285	6	AR014693 Sequence
2	441	100.0	285	6	AR432393 Sequence
3	441	100.0	288	6	A39553 Sequence 41

4	441	100.0	288	6	AR050161
5	441	100.0	288	6	AR130280
6	441	100.0	288	6	I23736 Sequence 58
7	433	98.2	285	6	AR014692 Sequence
8	433	98.2	285	6	AR432392 Sequence
9	433	98.2	395	15	RSU18557
10	433	98.2	414	6	A36875
11	433	98.2	414	6	A39549
12	433	98.2	414	6	A63404
13	433	98.2	414	6	AR050153
14	433	98.2	414	6	AR130272
15	433	98.2	414	6	I23728
16	433	98.2	414	6	AR207337
17	433	98.2	414	6	AR374914
18	433	98.2	414	6	AR642703
19	431	97.7	449	6	E34290
20	426	96.6	575	6	BD223249
21	425	96.4	457	15	RSU18556
22	405	91.8	243	15	AY998243
23	398	90.2	243	6	BD174927
24	398	90.2	414	6	E31545
25	398	90.2	414	15	AB012871
26	396.5	89.9	451	15	BNU59459
27	396	89.8	499	15	RSAPF4
28	395.5	89.7	475	15	RSEFP3
29	394	89.3	243	6	AX412329
30	394	89.3	243	6	AX412502
31	394	89.3	243	6	AX507351
32	394	89.3	243	6	AX590057
33	394	89.3	274	15	AY133787
34	394	89.3	400	6	A68647
35	394	89.3	454	15	AY063779
36	393	89.1	243	6	BD174928
37	393	89.1	363	15	AF528180
38	393	89.1	416	6	E31546
39	393	89.1	416	15	AB012872
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42	388	88.0	243	6	AX651878
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## ALIGNMENTS

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LOCUS	AR014693					
DEFINITION	AR014693					
ACCESSION	AR014693.1	GI:3972147				
VERSION	AR014693.1					
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 285)					
AUTHORS	Liang,J., Shah,D.Maganlal., Wu,Y.Shun. and Rosenberger,C.Annette.					
TITLE	Antifungal polypeptide and methods for controlling plant pathogenic fungi					
JOURNAL	Patent: US 5773696-A 17 30-JUN-1998;					
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Db 31 ATGGCTAAGTTTGGTCCCATCGCAGCTCTCTTTGCTGCTCTGCTCTCTTTGCTGCT 90
Qy 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTTP 40
Db 91 TTCGAGGCACCAACTATGTTGGTGGAGGCACAAAAGTTGTGCCAAGGCCATCAGGGACTTGG 150
Qy 41 SerGlyValCysGlyValAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60
Db 151 TCAGGAGTCTGCGGAACCAACACGCGATGCAAGACCAATGATCGATCTCGAAGAGGCA 210
Qy 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
Db 211 CGGCATGGATCTTGCAACTAGCTTTCCAGCTCACAAGTGCATCTGCTACTTTCCATGC 270

RESULT 2
AR432393
LOCUS                285 bp    DNA    linear    PAT 18-DEC-2003
DEFINITION           Sequence 17 from patent US 6653280.
ACCESSION             AR432393
VERSION               AR432393.1 GI:40194670
KEYWORDS
SOURCE                Unknown.
ORGANISM              Unclassified.
REFERENCE              1 (bases 1 to 285)
AUTHORS               Liang,J.,, Shah,D.M., Wu,Y.S. and Rosenberger,C.A.
TITLE                 Antifungal polypeptide AlyAPP from Alyssum and methods for
                     controlling plant pathogenic fungi
JOURNAL               Patent: US 6653280-A 17 25-NOV-2003;
                     Monsanto Technology LLC; St. Louis, MO
FEATURES
source
1..285
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Alignment Scores:      4,41e-44      Length:      285
Score:                441.00      Matches:      80
Percent Similarity:   100.0%      Conservative: 0
Best Local Similarity: 100.0%      Mismatches:  0
Query Match:         100.0%      Indels:       0
DB:                  6                Gaps:       0

US-09-759-584-59 (1-80) x AR432393 (1-285)

Qy 1 MetAlaLysPheAlaSerIleIleAlaLeuPheAlaAlaLeuValLeuPheAlaAla 20
Db 31 ATGGCTAAGTTTGGTCCCATCGCAGCTCTCTTTGCTGCTCTGCTCTCTTTGCTGCT 90
Qy 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTTP 40
Db 91 TTCGAGGCACCAACTATGTTGGTGGAGGCACAAAAGTTGTGCCAAGGCCATCAGGGACTTGG 150
Qy 41 SerGlyValCysGlyValAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60
Db 151 TCAGGAGTCTGCGGAACCAACACGCGATGCAAGACCAATGATCGATCTCGAAGAGGCA 210
Qy 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
Db 211 CGGCATGGATCTTGCAACTAGCTTTCCAGCTCACAAGTGCATCTGCTACTTTCCATGC 270

RESULT 3
AR432393
LOCUS                288 bp    DNA    linear    PAT 05-MAR-1997
DEFINITION           Sequence 41 from Patent WO9416076.
ACCESSION             A39553

```

```

VERSION            A39553.1 GI:2295844
KEYWORDS           unidentified
SOURCE            unidentified
ORGANISM           unclassified sequences.
REFERENCE          1 (bases 1 to 288)
AUTHORS            Dubock,A.C., Powell,K.A. and Rees,S.B.
TITLE             ANTIMICROBIAL-PROTEIN-PRODUCING ENDOSYMBIOTIC MICROORGANISMS
JOURNAL           Patent: WO 9416076-A 41 21-JUL-1994;
                     ZENECA LTD (GB)
COMMENT           Other publication AU 5820494 940815.
FEATURES
source
1..288
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

ORIGIN
Alignment Scores:      4,47e-44      Length:      288
Score:                441.00      Matches:      80
Percent Similarity:   100.0%      Conservative: 0
Best Local Similarity: 100.0%      Mismatches:  0
Query Match:         100.0%      Indels:       0
DB:                  6                Gaps:       0

US-09-759-584-59 (1-80) x A39553 (1-288)

Qy 1 MetAlaLysPheAlaSerIleIleAlaLeuPheAlaAlaLeuValLeuPheAlaAla 20
Db 43 ATGGCTAAGTTTGGTCCCATCGCAGCTCTCTTTGCTGCTCTGCTCTCTTTGCTGCT 102
Qy 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTTP 40
Db 103 TTCGAAGCACCACCAATGTTGGAAGCAGACAGAGTTGTGCCAAGGCCAAGTGGACATGG 162
Qy 41 SerGlyValCysGlyValAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60
Db 163 TCAGGAGTCTGTTGGAACCAATTAACGATGCAAGATCAGTGCATTAGACTTCGAGAAGCA 222
Qy 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
Db 223 CGCATGATGATCTTGCAACTATGCTCTCCAGCTCACAAGTGTATCTGCTACTTTCTGTT 282

RESULT 4
AR050161
LOCUS              Sequence 58 from patent US 5824869.
DEFINITION         AR050161
ACCESSION          AR050161
VERSION            AR050161.1 GI:5972153
KEYWORDS           Unknown.
SOURCE            Unknown.
ORGANISM           Unclassified.
REFERENCE          1 (bases 1 to 288)
AUTHORS            Broekaert W.F., Cammue B.P.A., Osborn,R.W., Rees,S.B.,
                     Terras,P.R.G. and Vanderleyden,J.
TITLE             Biocidal proteins
JOURNAL           Patent: US 5824869-A 58 20-OCT-1998;
                     Location/Qualifiers
FEATURES
source
1..288
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores:      4,47e-44      Length:      288
Score:                441.00      Matches:      80
Percent Similarity:   100.0%      Conservative: 0
Best Local Similarity: 100.0%      Mismatches:  0
Query Match:         100.0%      Indels:       0
DB:                  6                Gaps:       0

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US-09-759-584-59 (1-80) x AR050161 (1-288)

QY 1 MetalalysPheAlaSerIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 20  
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 Db 43 ATGGCTAAGTTTGGCTCCATCATCGCACTTCTTTTGGCTGCTCTTTTGGCTGCT 102  
 QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTrp 40  
 |||||  
 Db 103 TTCGAAGCACCAACAATGCTGGAAGCACAGAAAGTTGTGCCAAGGCCAAGTGGGACATGG 162  
 QY 41 SerGlyValCysGlyValAsnAsnAlaCysValysAsnGlnCysIleArgLeuGluLysAla 60  
 |||||  
 Db 163 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCAATAGACTTGGAGAAAGCA 222  
 QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80  
 |||||  
 Db 223 CGACATGGATCTTGCACATATGCTTCCAGCTCACAAGTGATCTGCTACTTCTTCTTGT 282

RESULT 5  
 AR130280 288 bp DNA linear PAT 16-MAY-2001  
 LOCUS  
 DEFINITION Sequence 58 from patent US 6187904.  
 ACCESSION AR130280  
 VERSION AR130280.1 GI:14118177

KEYWORDS  
 SOURCE Unknown.

ORGANISM Unknown.

REFERENCE Unclassified.

AUTHORS Broekaert,W.F., Cammue,B.P.A., Osborn,R.W., Rees,S.B.,  
 Terras,F.R.G. and Vanderleyden,J.  
 TITLE Biocidal proteins

JOURNAL Patent: US 6187904-A 58 13-FEB-2001;

FEATURES Location/Qualifiers

source 1..288

/organism="unknown"

/mol\_type="unassigned DNA"

ORIGIN

Alignment Scores:  
 Pred. No.: 4,47e-44 Length: 288  
 Score: 441.00 Matches: 80  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 100.0% Indels: 0  
 DB: 6 Gaps: 0

US-09-759-584-59 (1-80) x AR130280 (1-288)

QY 1 MetalalysPheAlaSerIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 20  
 |||||  
 Db 43 ATGGCTAAGTTTGGCTCCATCATCGCACTTCTTTTGGCTGCTCTTTTGGCTGCT 102  
 QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTrp 40  
 |||||  
 Db 103 TTCGAAGCACCAACAATGCTGGAAGCACAGAAAGTTGTGCCAAGGCCAAGTGGGACATGG 162  
 QY 41 SerGlyValCysGlyValAsnAsnAlaCysValysAsnGlnCysIleArgLeuGluLysAla 60  
 |||||  
 Db 163 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCAATAGACTTGGAGAAAGCA 222  
 QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80  
 |||||  
 Db 223 CGACATGGATCTTGCACATATGCTTCCAGCTCACAAGTGATCTGCTACTTCTTCTTGT 282

RESULT 6  
 I23736 288 bp DNA linear PAT 07-OCT-1996  
 LOCUS  
 DEFINITION Sequence 58 from patent US 5538525.  
 ACCESSION I23736  
 VERSION I23736.1 GI:1603606

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE Unclassified.

AUTHORS 1 (bases 1 to 288)

Terras,F.R.G. and Vanderleyden,J.  
 TITLE Biocidal proteins

JOURNAL Patent: US 5538525-A 58 23-JUL-1996;

FEATURES Location/Qualifiers

source 1..288

/organism="unknown"

/mol\_type="unassigned DNA"

ORIGIN

Alignment Scores:

Pred. No.: 4,47e-44 Length: 288  
 Score: 441.00 Matches: 80  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 100.0% Indels: 0  
 DB: 6 Gaps: 0

US-09-759-584-59 (1-80) x I23736 (1-288)

QY 1 MetalalysPheAlaSerIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 20  
 |||||  
 Db 43 ATGGCTAAGTTTGGCTCCATCATCGCACTTCTTTTGGCTGCTCTTTTGGCTGCT 102

QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTrp 40  
 |||||

Db 103 TTCGAAGCACCAACAATGCTGGAAGCACAGAAAGTTGTGCCAAGGCCAAGTGGGACATGG 162

QY 41 SerGlyValCysGlyValAsnAsnAlaCysValysAsnGlnCysIleArgLeuGluLysAla 60  
 |||||

Db 163 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCAATAGACTTGGAGAAAGCA 222

QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80  
 |||||

Db 223 CGACATGGATCTTGCACATATGCTTCCAGCTCACAAGTGATCTGCTACTTCTTCTTGT 282

RESULT 7

AR014692

LOCUS

DEFINITION Sequence 16 from patent US 5773696.

ACCESSION AR014692

VERSION AR014692.1

KEYWORDS GI:3972146

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE Unclassified.

AUTHORS 1 (bases 1 to 285)

Liang,J., Shah,D.Maganlal., Wu,Y.Shun. and Rosenberger,C.Annette.

TITLE Antifungal polypeptide and methods for controlling plant pathogenic

fungi

JOURNAL Patent: US 5773696-A 16 30-JUN-1998;

FEATURES Location/Qualifiers

source 1..285

/organism="unknown"

/mol\_type="unassigned DNA"

ORIGIN

Alignment Scores:

Pred. No.: 4,09e-43 Length: 285  
 Score: 433.00 Matches: 78  
 Percent Similarity: 98.8% Conservative: 1  
 Best Local Similarity: 97.5% Mismatches: 1  
 Query Match: 98.2% Indels: 0  
 DB: 6 Gaps: 0

US-09-759-584-59 (1-80) x AR014692 (1-285)

QY 1 MetalalysPheAlaSerIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 20  
 |||||

Db 31 ATGGCTAAGTTTGGCTCCATCATCGCACTCTTTTGGCTGCTCTTCTTCTTGTCTGCT 90

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QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTTP 40
Db 91 TTCGAGGACCAACTATGTTGGAGGACAAAAGTTGTGGAGAGGCCATCAGGACTTGG 150
QY 41 SerGlyValCysGlyAenAsnAenAlaCysLysAsnGlnCysIleAargLeuGluLysAla 60
Db 151 TCAGGAGTCTCGGAACAACAACGATGCAAGAACCAATGCATCAACCTCGAAGAGCA 210
QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
Db 211 CGGCATGGATCTTGGCAATACGTTCTCCAGCTCACAGTGCATCTGCTACTTTCATGC 270

RESULT 8
LOCUS AR432392 285 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 16 from patent US 6653280.
ACCESSION AR432392
VERSION AR432392.1 GI:40194669
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 285)
AUTHORS Liang,J., Shah,D.M., Wu,Y.S. and Rosenberger,C.A.
TITLE Antifungal polypeptide AlyAPP from Alyseum and methods for
controlling plant pathogenic fungi
JOURNAL Patent: US 6653280-A 16 25-NOV-2003;
Monsanto Technology LLC; St. Louis, MO
FEATURES
source
1..285
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Alignment Scores:
Pred. No.: 4,09e-43 Length: 285
Score: 433.00 Matches: 78
Percent Similarity: 98.8% Conservative: 1
Best Local Similarity: 97.5% Mismatches: 1
Query Match: 98.2% Indels: 0
DB: 6 Gaps: 0
US-09-759-584-59 (1-80) x AR432392 (1-285)

QY 1 MetAlaLysPheAlaSerIleIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 20
Db 31 ATGGCTAAGTTTGGTCCATCATCGCACCTCTTGTGCTCTCTGTTCTCTTTGCTGT 90
QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTTP 40
Db 91 TTCGAGGACCAACTATGTTGGAGGACAAAAGTTGTGGAGAGGCCATCAGGACTTGG 150
QY 41 SerGlyValCysGlyAenAsnAenAlaCysLysAsnGlnCysIleAargLeuGluLysAla 60
Db 151 TCAGGAGTCTCGGAACAACAACGATGCAAGAACCAATGCATCAACCTCGAAGAGCA 210
QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
Db 211 CGGCATGGATCTTGGCAATACGTTCTCCAGCTCACAGTGCATCTGCTACTTTCATGC 270

RESULT 9
RSU18557
LOCUS RSU18557 395 bp mRNA linear PLN 07-JUL-1995
DEFINITION Raphanus sativus antifungal protein 1 preprotein (Rs-AFP1) mRNA,
complete cds.
ACCESSION U18557
VERSION U18557.1 GI:644773
KEYWORDS Raphanus sativus (radish)
SOURCE Raphanus sativus
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

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rosids; eurosids II; Brassicales; Brassicaceae; Raphanus.
1 (sites)
Terras,F.R.G., Eggermont,K., Kovaleva,V., Raikhel,N.V.,
Osborn,R.W., Kessler,A., Rees,S.B., Torrekens,S., Van Leuven,F.,
Vanderleyden,J., Cammue,B.P.A. and Broekaert,W.F.
Small cysteine-rich antifungal proteins from radish: their role in
host defense
Plant Cell 7, 568-573 (1995)
2 (bases 1 to 395)
Terras,F.R.
Direct Submission
Submitted (14-DEC-1994) Franky R. Terras, F.A. Janssens Laboratory
of Genetics, Applied Biological Sciences, W. De Croylan 42,
Heverlee, Belgium, B-3001
On Feb 9, 1995 this sequence version replaced gi:609321.
FEATURES
source
1..395
/organism="Raphanus sativus"
/mol_type="mRNA"
/strain="ronde rode kleine witpunt"
/db_xref="taxon:3726"
/tissue_type="seed"
1..395
/gene="Rs-AFP1"
15..257
/gene="Rs-AFP1"
/function="antifungal, fungistatic"
/codon_start=1
/evidence=experimental
/product="antifungal protein 1 preprotein"
/protein_id="AAA69541.1"
/db_xref="GI:609322"
/translation="MAKFASTIIALLFAALVLFNAFAEAPTMEVAQKLCERPSTWSGVC
GNNAKKNQCINLEKARHGSCNVFFPAHKCIYFPC"
15..101
/gene="Rs-AFP1"
102..254
/gene="Rs-AFP1"
/product="antifungal protein 1"
/function="antifungal, fungistatic"
/note="Evidence for antifungal activity: Analysis of two
novel classes of antifungal proteins from radish (Raphanus
sativus L.) seeds. Terras, F.R.G. et al. (1992), J. Biol.
Chem. 267, 15301-15309"
/citation=[1]
/evidence=experimental
395
/gene="Rs-AFP1"
/note="18 A nucleotides"
polyA_signal
ORIGIN
Alignment Scores:
Pred. No.: 5,94e-43 Length: 395
Score: 433.00 Matches: 78
Percent Similarity: 98.8% Conservative: 1
Best Local Similarity: 97.5% Mismatches: 1
Query Match: 98.2% Indels: 0
DB: 15 Gaps: 0
US-09-759-584-59 (1-80) x RSU18557 (1-395)

QY 1 MetAlaLysPheAlaSerIleIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 20
Db 15 ATGGCTAAGTTTGGTCCATCATCGCACCTCTTGTGCTCTCTTGTGCTCTTTTGTGCTGT 74
QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTTP 40
Db 75 TTCGAGGACCAACAATGTTGGAGACACAGAGTTGTGGAAGGCCAAGTGGACATGG 134
QY 41 SerGlyValCysGlyAenAsnAenAlaCysLysAsnGlnCysIleAargLeuGluLysAla 60
Db 135 TCAGGAGTCTGTGGAAACAATAACGCATCGAAGATCATGTCATTAACCTTGAGAAGCA 194

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QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80  
Db 195 CGACATGGATCTTGCACACTATGCTTCCAGCTCACAAGTGTATCTGCTACTTCTCTGT 254

## RESULT 10

A26875 LOCUS R.sativus APF1 gene. 414 bp DNA linear PAT 30-NOV-2001  
DEFINITION A26875  
ACCESSION A26875  
VERSION A26875.1 GI:1247352  
KEYWORDS Raphanus sativus (radish)  
SOURCE Raphanus sativus  
ORGANISM Raphanus sativus  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids II; Brassicales; Brassicaceae; Raphanus.  
REFERENCE 1 (bases 1 to 414)  
AUTHORS Broekaert,W.F., Cammue,B.P.A., Terras,F.R.G., Vanderleyden,J.,  
Osborn,R.W. and Rees,S.B.  
TITLE BIOCIDAL PROTEINS  
JOURNAL Patent: WO 9305153-A 33 18-MAR-1993;  
ICI PLC (GB)

## FEATURES

source  
1..414  
Location/Qualifiers  
/organism="Raphanus sativus"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:3726"

## ORIGIN

Alignment Scores:  
Pred. No.: 6,27e-43 Length: 414  
Score: 433.00 Matches: 78  
Percent Similarity: 98.8% Conservative: 1  
Best Local Similarity: 97.5% Mismatches: 1  
Query Match: 98.2% Indels: 0  
DB: 6 Gaps: 0

US-09-759-584-59 (1-80) x A26875 (1-414)

QY 1 MetAlaLysPheAlaSerIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 20  
Db 16 ATGGCTAAGTTTGGCTCCATCATCGCACTCTTTTGTGCTCTTCTTTTGTCTGT 75  
QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTrp 40  
Db 76 TTCGAAGCACCACCAATGGTGGAAAGCACAGAAGTTGTGCGAAAGGCCAAGTGGGACATGG 135  
QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60  
Db 136 TCAGGAGTCTGTGGAAACAATACGCATGCAAGAATCAGTGCATTAAACCTTGAGAAAGCA 195  
QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80  
Db 196 CGACATGGATCTTGCACACTATGCTTCCAGCTCACAAGTGTATCTGCTACTTCTCTGT 255

## RESULT 11

A39549 LOCUS Sequence 37 from Patent WO9416076. 414 bp DNA linear PAT 05-MAR-1997  
DEFINITION A39549  
ACCESSION A39549  
VERSION A39549.1 GI:2295842  
KEYWORDS  
SOURCE unidentified  
ORGANISM unclassified sequences.  
REFERENCE 1 (bases 1 to 414)  
AUTHORS Dubock,A.C., Powell,K.A. and Rees,S.B.  
TITLE ANTIMICROBIAL-PROTEIN-PRODUCING ENDOSYMBIOTIC MICROORGANISMS  
JOURNAL Patent: WO 9416076-A 37 21-JUL-1994;  
ZENECA LTD (GB)  
COMMENT Other publication AU 5820494 940815.  
FEATURES  
source  
1..414  
Location/Qualifiers

/organism="unidentified"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"

## ORIGIN

Alignment Scores:  
Pred. No.: 6,27e-43 Length: 414  
Score: 433.00 Matches: 78  
Percent Similarity: 98.8% Conservative: 1  
Best Local Similarity: 97.5% Mismatches: 1  
Query Match: 98.2% Indels: 0  
DB: 6 Gaps: 0

US-09-759-584-59 (1-80) x A39549 (1-414)

QY 1 MetAlaLysPheAlaSerIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 20  
Db 16 ATGGCTAAGTTTGGCTCCATCATCGCACTCTTTTGTGCTCTTCTTTTGTCTGT 75  
QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTrp 40  
Db 76 TTCGAAGCACCACCAATGGTGGAAAGCACAGAAGTTGTGCGAAAGGCCAAGTGGGACATGG 135  
QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60  
Db 136 TCAGGAGTCTGTGGAAACAATACGCATGCAAGAATCAGTGCATTAAACCTTGAGAAAGCA 195  
QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80  
Db 196 CGACATGGATCTTGCACACTATGCTTCCAGCTCACAAGTGTATCTGCTACTTCTCTGT 255

## RESULT 12

A63404 LOCUS Sequence 19 from Patent WO9721814. 414 bp DNA linear PAT 12-MAR-1998  
DEFINITION A63404  
ACCESSION A63404  
VERSION A63404.1 GI:3717176  
KEYWORDS  
SOURCE unidentified  
ORGANISM unclassified sequences.  
REFERENCE 1  
AUTHORS Broekaert,W.F., De,S.G., Rees and Sarah,B.  
TITLE ANTI-FUNGAL PROTEINS  
JOURNAL Patent: WO 9721814-A 19 19-JUN-1997;  
ZENECA LTD (GB)  
COMMENT Other publication AU 1105397 19970703.  
FEATURES  
source  
1..414  
Location/Qualifiers  
/organism="unidentified"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"

## ORIGIN

Alignment Scores:  
Pred. No.: 6,27e-43 Length: 414  
Score: 433.00 Matches: 78  
Percent Similarity: 98.8% Conservative: 1  
Best Local Similarity: 97.5% Mismatches: 1  
Query Match: 98.2% Indels: 0  
DB: 6 Gaps: 0

US-09-759-584-59 (1-80) x A63404 (1-414)

QY 1 MetAlaLysPheAlaSerIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 20  
Db 16 ATGGCTAAGTTTGGCTCCATCATCGCACTCTTTTGTGCTCTTCTTTTGTCTGT 75  
QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTrp 40  
Db 76 TTCGAAGCACCACCAATGGTGGAAAGCACAGAAGTTGTGCGAAAGGCCAAGTGGGACATGG 135  
QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60

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Db 136 TCAGGAGTCTGTGGAAACATATAACGATGCATGCAAGATCAGTGCATTAACCTTGGAAAGCA 195
QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
Db 196 CGACATGGATCTTGCACACTATGTCTTCCAGCTCACAAGTGTATCTGCTACTTTCCTTGT 255

RESULT 13
AR050153
LOCUS AR050153 414 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 48 from patent US 5824869.
ACCESSION AR050153
VERSION AR050153.1 GI:5972145
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 414)
AUTHORS Broekaert, W.F., Cammue, B.P.A., Osborn, R.W., Rees, S.B.,
Terras, F.R.G. and Vanderleyden, J.
TITLE Biocidal proteins
JOURNAL Patent: US 5824869-A 48 20-OCT-1998;
FEATURES Location/Qualifiers
source 1..414
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.: 6.27e-43 Length: 414
Score: 433.00 Matches: 78
Percent Similarity: 98.8% Conservatives: 1
Best Local Similarity: 97.5% Mismatches: 1
Query Match: 98.2% Indels: 0
Gaps: 0

US-09-759-584-59 (1-80) x AR050153 (1-414)
QY 1 MetAlaLysPheAlaSerIleIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 20
Db 16 ATGGCTAAGTTTGGCTCCATCGCACTTCTTTTGGCTGCTCTTCTTTTGGCTGT 75
QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTTP 40
Db 76 TTCGAAGCACCACCAATATGTTGGAAAGCACAAGAGTTTGTGCGAAAGGCCAAGTGGACATGG 135
QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60
Db 136 TCAGGAGTCTGTGGAAACATATAACGATGCATGCAAGATCAGTGCATTAACCTTGGAAAGCA 195
QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
Db 196 CGACATGGATCTTGCACACTATGTCTTCCAGCTCACAAGTGTATCTGCTACTTTCCTTGT 255

RESULT 14
AR130272
LOCUS AR130272 414 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 48 from patent US 6187904.
ACCESSION AR130272
VERSION AR130272.1 GI:14118169
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 414)
AUTHORS Broekaert, W.F., Cammue, B.P.A., Osborn, R.W., Rees, S.B.,
Terras, F.R.G. and Vanderleyden, J.
TITLE Biocidal proteins
JOURNAL Patent: US 6187904-A 48 13-FEB-2001;
FEATURES Location/Qualifiers
source 1..414
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.: 6.27e-43 Length: 414
Score: 433.00 Matches: 78
Percent Similarity: 98.8% Conservatives: 1
Best Local Similarity: 97.5% Mismatches: 1
Query Match: 98.2% Indels: 0
Gaps: 0

US-09-759-584-59 (1-80) x AR050153 (1-414)
QY 1 MetAlaLysPheAlaSerIleIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 20
Db 16 ATGGCTAAGTTTGGCTCCATCGCACTTCTTTTGGCTGCTCTTCTTTTGGCTGT 75
QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTTP 40
Db 76 TTCGAAGCACCACCAATATGTTGGAAAGCACAAGAGTTTGTGCGAAAGGCCAAGTGGACATGG 135
QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60
Db 136 TCAGGAGTCTGTGGAAACATATAACGATGCATGCAAGATCAGTGCATTAACCTTGGAAAGCA 195
QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
Db 196 CGACATGGATCTTGCACACTATGTCTTCCAGCTCACAAGTGTATCTGCTACTTTCCTTGT 255

RESULT 15
AR130272
LOCUS AR130272 414 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 48 from patent US 5538525.
ACCESSION AR130272
VERSION AR130272.1 GI:1603598
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 414)
AUTHORS Broekaert, W.F., Cammue, B.P.A., Osborn, R.W., Rees, S.B.,
Terras, F.R.G. and Vanderleyden, J.
TITLE Biocidal proteins
JOURNAL Patent: US 5538525-A 48 23-JUL-1996;
FEATURES Location/Qualifiers
source 1..414
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.: 6.27e-43 Length: 414
Score: 433.00 Matches: 78
Percent Similarity: 98.8% Conservatives: 1
Best Local Similarity: 97.5% Mismatches: 1
Query Match: 98.2% Indels: 0
Gaps: 0

US-09-759-584-59 (1-80) x I23728 (1-414)
QY 1 MetAlaLysPheAlaSerIleIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 20
Db 16 ATGGCTAAGTTTGGCTCCATCGCACTTCTTTTGGCTGCTCTTCTTTTGGCTGT 75
QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTTP 40
Db 76 TTCGAAGCACCACCAATATGTTGGAAAGCACAAGAGTTTGTGCGAAAGGCCAAGTGGACATGG 135
QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60
Db 136 TCAGGAGTCTGTGGAAACATATAACGATGCATGCAAGATCAGTGCATTAACCTTGGAAAGCA 195
QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
Db 196 CGACATGGATCTTGCACACTATGTCTTCCAGCTCACAAGTGTATCTGCTACTTTCCTTGT 255
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Db 196 CGACATGGATCTTGCACACTATGTCTTCCAGCTCACAGTGTATCTGTACTTCTTCTTGT 255

Search completed: May 10, 2006, 08:02:43  
Job time : 3630 secs

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GenCore version 5.1.1.8  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: May 10, 2006, 05:44:15 ; Search time 452 Seconds  
(without alignments)  
1769.387 Million cell updates/sec

Title: US-09-759-584-59  
Perfect score: 441  
Sequence: 1 MAKFAIIALLPAULVFAA.....RHGSCNYYVPAHKICICYPCC 80

Scoring table: BLASTUM62

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss03h  
-USER=US09759584 @CGN 1.1 900 @runat\_08052006\_175226\_11223 -NCPU=6 -ICPU=3  
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-WARN\_TIMEOUT=30 -THREADS=1 -XGAPEXT=0.5 -YGAPEXT=0.5 -DELOP=6 -FGAPEXT=7  
-YGAPEXT=10 -YGAPEXT=0.5 -DELOP=6 -DBLEXT=7

Database : N\_Geneseq.21.\*

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- 3: Geneseqn2000s.\*
- 4: Geneseqn2001as.\*
- 5: Geneseqn2001bs.\*
- 6: Geneseqn2002as.\*
- 7: Geneseqn2002bs.\*
- 8: Geneseqn2003as.\*
- 9: Geneseqn2003bs.\*
- 10: Geneseqn2003cs.\*
- 11: Geneseqn2003ds.\*
- 12: Geneseqn2004as.\*
- 13: Geneseqn2004bs.\*
- 14: Geneseqn2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	441	100.0	261	2	Aaq38652 Rs-APP2 c
2	441	100.0	288	2	Aaq70130 Antimicro
3	433	98.2	414	2	Aaq38650 Rs-APP1 c
4	433	98.2	414	2	Aaq70128 Antimicro

5	433	98.2	414	2	AAT72333	Aat72333 Raphanus
6	433	98.2	414	2	AAT68696	Aat68696 Radish an
7	431	97.7	449	3	AAA53190	Aaa53190 Raphanus
8	426	96.6	575	3	AAZ99339	Aaz99339 DNA encod
9	423	95.9	394	10	ADC51221	Adc51221 Brassica
10	423	95.9	394	13	ADU71300	Adu71300 Brassica
11	416	94.3	426	10	ADC51223	Adc51223 Brassica
12	416	94.3	426	13	ADU71302	Adu71302 Brassica
13	398	90.2	243	6	ABQ82690	Abq82690 Wasabia j
14	398	90.2	243	3	AAZ39123	Aaz39123 Wasabia j
15	394	89.3	243	6	ABZ14241	Abz14241 Arabidops
16	394	89.3	243	6	ADG87651	Adg87651 A. thalia
17	394	89.3	243	6	ADG87824	Adg87824 A. thalia
18	394	89.3	243	8	ABZ42136	Abz42136 Arabidops
19	394	89.3	400	2	AAV10633	Aav10633 A. thalia
20	394	89.3	400	7	ADZ75091	Adz75091 Arabidops
21	393	89.1	243	6	ABQ82691	Abq82691 Wasabia j
22	393	89.1	416	3	AAZ39124	Aaz39124 Wasabia j
23	388	88.0	243	6	ADG87728	Adg87728 A. thalia
24	388	88.0	243	8	ADA68378	Ada68378 Arabidops
25	388	88.0	243	8	AAV10632	Aav10632 A. thalia
26	387.5	87.9	270	2	AAT94582	Aat94582 Amplified
27	387.5	87.9	286	2	AAT94574	Aat94574 Alyssum s
28	387.5	87.9	481	2	AAT99289	Aat99289 Alyssum s
29	386	87.5	308	2	AAT94577	Aat94577 Cloned 5'
30	375	85.0	500	2	AAT94581	Aat94581 Composite
31	350	79.4	1973	3	AAZ46924	Aaz46924 Arabidops
32	349	79.1	1616	2	AAV10646	Aav10646 A. thalia
33	312	70.7	159	10	ADG32304	Adg32304 Radish cd
34	312	70.7	984	10	ADG32343	Adg32343 DNA encod
35	312	70.7	987	10	ADG32350	Adg32350 DNA encod
36	312	70.7	987	10	ADG32348	Adg32348 DNA encod
37	311	70.5	534	3	AAZ99327	Aaz99327 DNA encod
38	309.5	70.2	522	3	AAZ99324	Aaz99324 DNA encod
39	309	70.1	485	3	AAZ99333	Aaz99333 DNA encod
40	309	70.1	1093	3	AAZ99334	Aaz99334 DNA encod
41	308	69.8	534	3	AAZ51396	Aaz51396 Portion o
42	308	69.8	534	3	AAZ99325	Aaz99325 DNA encod
43	308	69.8	606	3	AAZ99326	Aaz99326 DNA encod
44	301	68.3	153	13	ADR39338	Adr39338 Defensin-

ALIGNMENTS

RESULT 1  
AAQ38652  
ID AAQ38652 standard; DNA; 261 BP.  
XX  
AC AAQ38652;  
DT 25-MAR-2003 (revised)  
DT 07-JUL-1993 (first entry)  
XX  
DE Rs-APP2 cDNA.  
XX  
KW Raphanus sativus; Brassica; Arabidopsis; Cnicus; Lathyrus; Clitoria;  
KW fungicide; bactericide; antibiotic; antifungal; gram positive;  
KW plant disease resistance; low toxicity.  
XX  
OS Raphanus sativus.  
XX  
FH Key Location/Qualifiers  
FT CDS 16..256  
FT /\*tag= a  
XX  
PN WO9305153-A1.  
PD 18-MAR-1993.  
XX  
XX 27-AUG-1992; 92WO-GB001570.  
XX  
PR 29-AUG-1991; 91GB-00018523.

```

PR 13-FEB-1992; 92GB-00003038.
PR 25-JUN-1992; 92GB-00013526.
XX
XX (ICIL ) IMPERIAL CHEM IND PLC.
XX
XX Broekaert WF, Cammue BPA, Osborn RW, Rees SB, Terras FRG;
PI Vanderleyden J;
XX
XX WPI; 1993-100978/12.
XX
XX Biocidal proteins isolated from seeds of plants - e.g. brassica or
PT dahlia, useful for increasing plants' resistance to fungal and bacterial
PT diseases.
XX
XX Example 21; Fig 35; 110pp; English.
XX
XX This cDNA represents the sequence of Rs-APP2 from Raphanus sativus. PCR
CC primer AAQ38640 was used together with AAQ38641 to generate a probe for
CC screening a Raphanus sativus seed cDNA library. This primer corresponds
CC to amino acids 2 to 7 of Rs-APPI and has a sense orientation. The 144bp
CC product was partially re-amplified using AAQ38642 and AAQ38641 to give a
CC 123bp product, which was further reamplified with the same primers and
CC digoxigenin-11-dUTP instead of dTTP to give a digoxigenin labeled PCR
CC product. This was used to screen a lambda ZAPII cDNA library by in situ
CC plaque hybridisation. Positive plaques were purified and subjected to two
CC additional screening rounds with the same probe. Inserts were excised in
CC vivo into the pBluescript phagemid form with the aid of helper phage
CC K408. Inserts from 22 positive clones were excised by EcoRI digestion and
CC their size compared by agarose gel electrophoresis. Four clones had
CC insert sizes of approx. 400bp the others between 250-300bp. The inserts
CC of the 4 largest clones were then sequenced and found to differ only in
CC the length of their 5' and 3' UTR's. The longest sequence was identified
CC as Rs-APPI (AAQ38650). Rs-APP2 was seen to differ by only 2 amino acids
CC from Rs-APPI, so the Rs-APPI cDNA was transformed to the Rs-APP2
CC nucleotide sequence by PCR assisted site directed mutagenesis. (Updated
CC on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 261 BP; 67 A; 55 C; 59 G; 80 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 8-76e-45 Length: 261
Score: 441.00 Matches: 80
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

US-09-759-584-59 (1-80) x AAQ38652 (1-261)
QY 1 MetAlaIyPheAlaSerIleIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 20
DB 16 ATGGCTAAGTTTGGGTCCATCATCGCACTTCTTTTGTGCTCTCTTTCTTTTGTGCT 75
QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTrp 40
DB 76 TTCGAGCACCACCAATGTTGGTGAAGCACAGAGTGTGTCACAAAGGCCAAGTGGGACATGG 135
QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60
DB 136 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAAATCAGTGCATTAGACTTGAAGAAGCA 195
QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
DB 196 CGACATGGATCTTGGCAACTAATGCTTCCAGCTCACAAGTGTATCTGCTACTTCTTCTTGT 255

RESULT 2
AAQ70130
ID AAQ70130 standard; cDNA; 288 BP.
XX
XX AAQ70130;
XX
XX 25-MAR-2003 (revised)
DT 14-FEB-1995 (first entry)

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XX Antimicrobial Rs-APP2.
DE
XX Antimicrobial; Rs-APP2; symbiosis; disease-resistance; fungus-resistance;
KW Clavibacter xyli subsp. cynodontis; Cxc; crop improvement; endophyte;
KW PCR; polymerase chain reaction; mutagenesis; ss.
XX
XX Raphanus sativus.
OS
XX
XX WO9416076-A1.
PN
XX
XX 21-JUL-1994.
PD
XX
XX 05-JAN-1994; 94WO-GB0000012.
PF
XX
XX 08-JAN-1993; 93GB-00000281.
PR
XX
XX (ZENE ) ZENECA LTD.
PA
XX
XX Dubock AC, Powell KA, Rees SB;
PI
XX
XX WPI; 1994-249223/30.
DR
XX P-PSDB; AAR57327.
DR
XX
XX Antimicrobial protein producing endo-symbiotic microorganisms - is
PT produced by combining nucleic acids encoding the protein with an
PT endophyte, useful for protecting plant hosts from esp. fungal disease.
XX
XX Disclosure; Page 33; 39pp; English.
XX
XX Plant-derived antimicrobial proteins are expressed in endosymbiotic
CC Clavibacter xyli subsp. cynodontis (Cxc). Plants or seeds treated with
CC recombinant Cxc are protected against fungal disease. A suitable
CC antimicrobial protein is Rs-APPI from R. sativus. The full-length cDNA
CC sequence of PCR assisted site-directed mutagenesis of Rs-APP2 is given in
CC AAQ70130 and the deduced amino acid sequence in AAR57327. (Updated on 25-
CC MAR-2003 to correct PN field.)
XX
XX Sequence 288 BP; 70 A; 66 C; 69 G; 83 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1e-44 Length: 288
Score: 441.00 Matches: 80
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

US-09-759-584-59 (1-80) x AAQ70130 (1-288)
QY 1 MetAlaIyPheAlaSerIleIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 20
DB 43 ATGGCTAAGTTTGGGTCCATCATCGCACTTCTTTTGTGCTCTCTTTTGTGCTGTCT 102
QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTrp 40
DB 103 TTCGAGCACCACCAATGTTGGTGAAGCACAGAGTGTGTCACAAAGGCCAAGTGGGACATGG 162
QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60
DB 163 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAAATCAGTGCATTAGACTTGAAGAAGCA 222
QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
DB 223 CGACATGGATCTTGGCAACTAATGCTTCCAGCTCACAAGTGTATCTGCTACTTCTTCTTGT 282

RESULT 3
AAQ38650
ID AAQ38650 standard; DNA; 414 BP.
XX
XX AAQ38650;
XX
XX 25-MAR-2003 (revised)
DT

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DT 07-JUL-1993 (first entry)
DE Re-APF1 cDNA.
XX
XX Raphanus sativus; Brassica; Arabidopsis; Cnicus; Lathyrus; Clitoria;
KW fungicide; bactericide; antibiotic; antifungal; gram positive;
KW plant disease resistance; low toxicity.
XX
XX Raphanus sativus.
OS
XX
XX Key Location/Qualifiers
FH 16..256
FT /*tag= a
FT
XX
XX W09305153-A1.
XX
XX 18-MAR-1993.
XX
XX 27-AUG-1992; 92WO-GB001570.
XX
XX 29-AUG-1991; 91GB-00018523.
PR 13-FEB-1992; 92GB-00003038.
PR 25-JUN-1992; 92GB-00013526.
XX
XX (ICIL ) IMPERIAL CHEM IND PLC.
PA
XX
XX Broekaert WF, Cammue BPA, Osborn RW, Rees SB, Terras FRG;
PI Vanderleyden J;
PI
XX
XX WPI; 1993-100978/12.
XX
XX Biocidal proteins isolated from seeds of plants - e.g. brassica or
PT dahlia, useful for increasing plants' resistance to fungal and bacterial
PT diseases.
XX
XX
XX Example 21; Fig 35; 110pp; English.
XX
XX This cDNA represents the sequence of Rs-APF1 from Raphanus sativus. PCR
CC primer AAQ38640 was used together with AAQ38641 to generate a probe for
CC screening a Raphanus sativus seed cDNA library. This primer corresponds
CC to amino acids 2 to 7 of Rs-APF1 and has a sense orientation. The 144bp
CC product was partially re-amplified using AAQ38642 and AAQ38641 to give a
CC 123bp product, which was further reamplified with the same primers and
CC digoxigenin-11-dUTP instead of dTTP to give a digoxigenin labeled PCR
CC product. This was used to screen a lambda ZAPII cDNA library by in situ
CC plaque hybridisation. Positive plaques were purified and subjected to two
CC additional screening rounds with the same probe. Inserts were excised in
CC vivo into the pBluescript phagemid form with the aid of helper phage
CC R408. Inserts from 22 positive clones were excised by EcoRI digestion and
CC their size compared by agarose gel electrophoresis. Four clones had
CC insert sizes of approx. 400bp the others between 250-300bp. The inserts
CC of the 4 largest clones were then sequenced and found to differ only in
CC the length of their 5' and 3' UTR's. The longest sequence is given here.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1,55e-43 Length: 414
Score: 433.00 Matches: 78
Percent Similarity: 98.8% Conservative: 1
Best Local Similarity: 97.5% Mismatches: 1
Query Match: 98.2% Indels: 0
DB: 2 Gaps: 0

US-09-759-584-59 (1-80) x AAQ38650 (1-414)

QY 1 MetAlaLysPheAlaSerIleAlaLeuPheAlaAlaLeuValLeuPheAlaAla 20
DB 16 ATGGCTAAGTTGGCTCCATCGCAGCTCTCTTTTGGCTGCTCTTTTGGCTGCT 75
QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTrp 40
DB 76 TTCGAAGCACCACCAATGGTGGAGAGTTGTGCGAAGGCTCAAGTGGGACATGG 135

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QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60  
 Db 136 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGATCAGTGATTAACCTTGAGAAAGCA 195

QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80  
 Db 196 CGACATGGATCTGTGCAACTATGCTTCCAGGCTCACAGTGTATCTGCTACTTCTTGT 255

RESULT 5  
 AAT72333  
 ID AAT72333 standard; cDNA; 414 BP.  
 XX  
 AC AAT72333;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 19-JAN-1998 (first entry)  
 XX  
 DE Raphanus sativus antifungal protein I (Rs-APP1) cDNA.  
 XX  
 KW Antifungal protein; candida; fungal resistance; food additive; radish;  
 KW crop protection; plant defensin; bacterial protection; preservative; ss.  
 XX  
 OS Raphanus sativus.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 16..258  
 FT /\*tag= a  
 FT /transl\_except= (pos:85..87, aa:Glu)  
 FT sig\_peptide 16..102  
 FT /\*tag= b  
 FT mat\_peptide 103..255  
 FT /\*tag= c  
 FT /product= "antifungal\_protein\_1"  
 FT  
 FT  
 XX WO9721815-A2.  
 XX  
 XX 19-JUN-1997.  
 PD  
 XX  
 XX 12-DEC-1996; 96WO-GB003068.  
 XX  
 XX 13-DEC-1995; 95GB-00025455.  
 PR 28-MAR-1996; 96GB-00006552.  
 XX  
 XX (ZENE ) ZENECA LTD.  
 PA  
 XX  
 XX Meloen RH, Puijk WC, Schaaper WM, Sijtsma L, Van Amerongen A;  
 PI Broekaert W, Samblanx GW, Fant F, Borremans FAM, Rees SB;  
 PI Van Gelder WMJ;  
 XX  
 XX WPI; 1997-332786/30.  
 DR P-PSDB; AAW19280.  
 DR  
 XX  
 XX Antifungal peptide derived from radish antifungal protein 2 - and related  
 PT DNA, useful for producing plants with increased fungal resistance and as  
 PT therapeutic or preservative agent.  
 PT  
 XX  
 XX Claim 8; Fig 2; 65pp; English.  
 PS  
 XX  
 XX This cDNA sequence encodes a Raphanus sativus (radish) antifungal  
 CC protein (Rs-APP1). Analogues of the homologous protein, Rs-APP2  
 CC (AAW19281), have also been produced (see AAW19282-92, AAW19294-98,  
 CC AAW19301-04, AAW1930-34 and AAW1765-834). Plants containing DNA  
 CC sequences encoding these proteins have improved resistance to fungi.  
 CC Compositions containing the peptides can be used to control fungi or  
 CC bacteria in pharmaceutical (e.g. treatment of Candida infections) or  
 CC preservative purposes (as food additives). In agriculture, the peptide  
 CC may be used to improve disease resistance or disease tolerance of crops,  
 CC either pre or post harvest. When applied to plants they may also have  
 CC curative as well as protective actions. The peptides may also be used to  
 CC protect plants by introducing them, or a microorganism capable of  
 CC expressing the peptide into the soil. (Updated on 25-MAR-2003 to correct  
 CC PI field.)

XX  
 SQ Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 1.55e-43 Length: 414  
 Score: 433.00 Matches: 78  
 Percent Similarity: 98.8% Conservative: 1  
 Best Local Similarity: 97.5% Mismatches: 1  
 Query Match: 98.2% Indels: 0  
 DB: 2 Gaps: 0

US-09-759-584-59 (1-80) x AAT72333 (1-414)  
 QY 1 MetAlaLysPheAlaSerIleAlaLeuLeuPheAlaLeuValLeuPheAlaLa 20  
 Db 16 ATGGCTAAGTTGCGTCCATCATCGCACTCTTTTTCGCTCTTGTCTTTTGTGCTGT 75  
 QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTrp 40  
 Db 76 TTCGAAGCACCAACAATGTTGGGAAGCACAGAAAGTTGTGCAAGGCCCAAGTGGGACATGG 135  
 QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60  
 Db 136 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGATCAGTGATTAACCTTGAGAAAGCA 195  
 QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80  
 Db 196 CGACATGGATCTGTGCAACTATGCTTCCAGGCTCACAGTGTATCTGCTACTTCTTGT 255

RESULT 6  
 AAT68696  
 ID AAT68696 standard; cDNA; 414 BP.  
 XX  
 AC AAT68696;  
 XX  
 DT 13-DEC-1997 (first entry)  
 XX  
 DE Radish antifungal protein 1 (Rs-APP1) cDNA.  
 XX  
 KW Rs-APP1; radish antifungal protein 1; fungicide; salt tolerance;  
 KW preservative; transgenic plant; crop protection.  
 XX  
 OS Raphanus sativus.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 16..258  
 FT /\*tag= a  
 FT /transl\_except= (pos:85..87, aa:Glu)  
 FT sig\_peptide 16..102  
 FT /\*tag= b  
 FT mat\_peptide 103..255  
 FT /\*tag= c  
 FT  
 FT  
 XX WO9721814-A1.  
 PN  
 XX  
 XX 19-JUN-1997.  
 PD  
 XX  
 XX 12-DEC-1996; 96WO-GB003065.  
 XX  
 XX 13-DEC-1995; 95GB-00025474.  
 PR (ZENE ) ZENECA LTD.  
 PA  
 XX Broekaert WF, De Samblanx GW, Rees SB;  
 XX WPI; 1997-332785/30.  
 DR P-PSDB; AAW19617.  
 XX  
 XX New active mutants of radish antifungal protein 2 - used to generate  
 PT fungus-resistant plants or as therapeutic or preservative agents.  
 PT  
 XX Disclosure; Fig 2; 39pp; English.  
 XX

CC This cDNA clone codes for the preprotein for the radish antifungal protein 1 (Rs-APP1) (AAW19617). Novel antifungal proteins are based on Rs-APP1, Rs-APP2 (see AAW19616), Rs-APP3 and Rs-APP4, especially those in which Gly9 is replaced by Arg, Val39 by Arg, Gly9 by Arg, Glu5 by Met and/or Gly16 by Met. Mutants (see AAW26371-90) of Rs-APP2 are specifically claimed. The CC mutants show improved salt tolerant antifungal activity, particularly CC when expressed in plants

XX Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;

Alignment Scores: 1.55e-43 Length: 414  
 Pred. No.: 433.00 Matches: 78  
 Score: 98.8% Conservative: 1  
 Percent Similarity: 97.5% Mismatches: 1  
 Best Local Similarity: 98.2% Indels: 0  
 Query Match: 2 Gaps: 0  
 DB:

US-09-759-584-59 (1-80) x AAT68696 (1-414)

QY 1 MetAlaLysPheAlaSerIleIleAlaLeuPheAlaAlaLeuValLeuPheAlaAla 20  
 DB 16 ATGGCTAAGTTGGTCCATCGCACTCTTTTGGCTGCTTGTCTTTTGGCTGT 75  
 QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTrp 40  
 DB 76 TTCGAAGCACCACCAATGTTGGGAAGCACAGAGTGTGCGAAGGCCAAGTGGGACATGG 135  
 QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60  
 DB 136 TCAGGAGTCTGTGGAAACAATACGCATCGCAAGATCAAGTGCATTAACCTTGAGGAAGCA 195  
 QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80  
 DB 196 CGACATGGATCTTGCACATAGTCTCCAGCTCACAAGTGTATCTGCTACTTCTTCTGT 255

#### RESULT 7

AAZ53190  
 ID AAZ53190 standard; DNA; 449 BP.  
 XX  
 AC AAZ53190;  
 XX  
 DT 06-OCT-2000 (first entry)  
 XX  
 DE Raphanus sativus antibacterial protein radishin encoding DNA SEQ ID NO:1.  
 XX  
 KW Raphanus sativus; antibacterial; plant; resistance; paddy; radishin;  
 KW pathogenic microbe; radish; rice blast disease; ds.  
 XX  
 OS Raphanus sativus.  
 XX  
 JP2000116379-A.  
 XX  
 PD 25-APR-2000.  
 XX  
 PF 09-OCT-1998; 98JP-00288472.  
 XX  
 PR 09-OCT-1998; 98JP-00288472.  
 XX  
 PA (TOYA-) TOYAMA KEN.  
 XX  
 WIPI; 2000-389821/34.  
 DR P-PSDB; AAY91117.  
 XX

Isolated DNA from Raphanus sativus used to transform a microbe and a plant to produce an antibacterial protein used to increase resistance of rice paddy against pathogenic microbes.

Claim 1; Page 4; 7pp; Japanese.

The present sequence encodes an antibacterial protein, designated radishin, isolated from Raphanus sativus (radish). A phage or plasmid comprising radishin can be used for increasing resistance of paddy and

CC rice blast disease against pathogenic microbes  
 XX Sequence 449 BP; 126 A; 78 C; 94 G; 151 T; 0 U; 0 Other;

Alignment Scores: 3.04e-43 Length: 449  
 Pred. No.: 431.00 Matches: 77  
 Score: 98.8% Conservative: 2  
 Percent Similarity: 96.2% Mismatches: 1  
 Best Local Similarity: 97.7% Indels: 0  
 Query Match: 3 Gaps: 0  
 DB:

US-09-759-584-59 (1-80) x AAA53190 (1-449)

QY 1 MetAlaLysPheAlaSerIleIleAlaLeuPheAlaAlaLeuValLeuPheAlaAla 20  
 DB 41 ATGGCTAAGTTGGTCCATCATCTCTTCTCGCTGCTCTTGTCTGCTTTTCTGCT 100  
 QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTrp 40  
 DB 101 TTCGAAGCACCACCAATGTTGGGAAGCACAGAGTGTGTCTCAGAGGCCAAGTGGGACATGG 160  
 QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60  
 DB 161 TCAGGAGTCTGTGGAAATTAATAACGATCGCAAGATCAAGTGCATTCGACTTGAGGAAGCA 220  
 QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80  
 DB 221 CGACATGGTCTTGCACATAGTCTTCCAGCTCACAAGTGTATCTGTTATTTCCCTTGT 280

#### RESULT 8

AAZ99339  
 ID AAZ99339 standard; DNA; 575 BP.  
 XX  
 AC AAZ99339;  
 XX  
 DT 03-JUL-2000 (first entry)  
 XX  
 DE DNA encoding a fusion protein of DmAMP1 and RsAPP2.  
 XX  
 KW Antimicrobial protein; AMP1; transgenic plant; linker peptide;  
 KW protein expression; plant defensin; RsAPP2; antifungal protein; APP2; ss.  
 XX  
 OS Synthetic.  
 OS Dahlia merckii.  
 OS Unidentified.  
 XX  
 FH Key Location/Qualifiers  
 CDS 3..566  
 FT /\*tag= a  
 FT /product= "fusion protein of DmAMP1 and RsAPP2"  
 XX  
 WO200011175-A1.  
 XX  
 PD 02-MAR-2000.  
 XX  
 PF 17-AUG-1999; 99WO-GB002716.  
 XX  
 PR 18-AUG-1998; 98GB-00018001.  
 PR 04-DEC-1998; 98GB-00026753.  
 XX  
 PA (ZENB ) ZENECA LTD.  
 XX  
 PI Broekaert WF, Francois IEJA, De Bolle MFC, Evans IJ, Ray JA;  
 XX  
 WIPI; 2000-246564/21.  
 DR P-PSDB; AAY84072.  
 XX  
 PT Improving expression of polyproteins in plants involves coexpression of  
 PT two or more proteins in plants within a single transcription unit.  
 XX  
 PS Disclosure; Fig 34; 151pp; English.  
 XX

CC The present sequence encodes a protein of the invention, comprising the  
 CC mature proteins of the plant defensin, the Dahlia antimicrobial protein  
 CC (AMP) 1 and the antifungal protein 2 (RafP2), linked by a linker  
 CC propeptide of the invention. The specification describes methods for  
 CC improving expression levels of one or more proteins in a transgenic  
 CC plant. The method comprises inserting a DNA sequence having a promoter  
 CC region operably linked to two or more protein encoding regions separated  
 CC by a DNA sequence coding for a linker propeptide and a terminator region.  
 CC The method is used to produce proteins in plants. The linker propeptide  
 CC comprising a cleavage site, whereby the expressed polypeptide is post-  
 CC translationally processed into the component protein molecules. The  
 CC propeptide sequence is rich in amino acids A, V, S and T and contains  
 CC dipeptidic sequences consisting of either two acidic, two basic or one  
 CC acidic and one basic residue as a cleavable linker sequence  
 XX  
 SQ Sequence 575 BP; 133 A; 137 C; 149 G; 156 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 1,73e-42 Length: 575  
 Score: 426.00 Matches: 78  
 Percent Similarity: 97.5% Conservative: 0  
 Best Local Similarity: 97.5% Mismatches: 2  
 Query Match: 96.6% Indels: 0  
 DB: 3 Gaps: 0

US-09-759-584-59 (1-80) x AA299339 (1-575)

QY 1 MetAlaLysPheAlaSerIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 20  
 DB 324 ATGGCTAAGTTTGGCGTCCATCATCGCACTTCTTTTTCGCTGCTGCTTCTTTTTCGCTGCT 383  
 QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTTP 40  
 DB 384 TTCGAAGCACCACCAATGTTGGAAGCACAGAAGTTGTGCCAAGGCCAAGTCGTACATGG 443  
 QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60  
 DB 444 TCAGGAGTCTGTGGAAACAAATACGATCGCAAGATCAGTCATAGACTTCGGAAGCA 503  
 QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80  
 DB 504 CGACATGGATCTTGCAACTATCGTTTCCAGCTCACAAGTGATCTGCTACTTTCCTTGT 563

RESULT 9

ADCS1221  
 ID ADCS1221 standard; DNA; 394 BP.

AC ADCS1221;

DT 18-DEC-2003 (first entry)

DE Brassica oleracea defensin protein coding sequence.

XX antimicrobial protein; defensin; transgenic plant;  
 XX composite disease resistance; pathogenic bacteria;  
 XX rice white leaf blight; brown-stripe disease; glume blight;  
 XX seedling damping-off disease; filamentous fungi; rice blight;  
 XX sheath blight disease; leaf blight; gene; ds.

OS Brassica oleracea.

PH Key Location/Qualifiers  
 FT CDS 1..243

FT /\*tag= a  
 FT /product= "Brassica oleracea defensin protein"

XX JP2003088379-A.

XX 25-MAR-2003.

XX 18-SEP-2001; 2001JP-00283117.

XX 18-SEP-2001; 2001JP-00283117.

XX  
 PA  
 XX  
 DR  
 DR  
 XX  
 PT  
 PT  
 PT  
 XX  
 PS  
 XX  
 CC  
 CC  
 CC  
 CC  
 CC  
 CC  
 CC  
 CC  
 CC  
 SQ  
 Alignment Scores:  
 Pred. No.: 2,43e-42 Length: 394  
 Score: 423.00 Matches: 76  
 Percent Similarity: 96.2% Conservative: 1  
 Best Local Similarity: 95.0% Mismatches: 3  
 Query Match: 95.9% Indels: 0  
 DB: 10 Gaps: 0  
 US-09-759-584-59 (1-80) x ADCS1221 (1-394)  
 QY 1 MetAlaLysPheAlaSerIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 20  
 DB 1 ATGGCTAAGTTTGTGCTCCATCATTCGCTTCTTTTTCGCTGCTTCTTTTTCGCTGCT 60  
 QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTTP 40  
 DB 61 CTCGAAGCACCACCAATGTTGGAAGCACAGAAGTTGTGCGAAGGCCAAGTCGGAACATGG 120  
 QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60  
 DB 121 TCAGGAGTCTGTGGAAACAAATACGATCGCAAGATCAGTCATTAACCTTCGGAAGCA 180  
 QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80  
 DB 181 CGACATGGATCTTGCAACTATGCTTCCAGCTCACAAGTGATTTTGTCTACTTCCCTTGT 240  
 RESULT 10  
 ADU71300  
 ID ADU71300 standard; cDNA; 394 BP.  
 XX  
 AC ADU71300;  
 XX  
 DT 10-FEB-2005 (first entry)  
 XX  
 DE Brassica oleracea defensin protein coding sequence - SEQ ID 1.  
 XX antimicrobial; plant disease resistance; gene; ss; defensin.  
 OS Brassica oleracea.  
 XX  
 PH Key Location/Qualifiers  
 FT CDS 1..243  
 FT /\*tag= a  
 FT /product= "Brassica oleracea defensin protein - SEQ ID 2"  
 XX  
 XX  
 PN JP2004329215-A.  
 XX  
 PD 25-NOV-2004.  
 XX

(DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.

WPI; 2003-621123/59.

P-PSDB; ADCS1222.

Novel protein from Brassica campestris, useful as antimicrobial against plant pathogenic filamentous fungi or pathogenic bacteria, especially for treating e.g. rice white leaf blight and sheath blight disease.

Claim 3; SEQ ID NO 1; 34pp; Japanese.

The invention comprises the amino acid and coding sequences of antimicrobial (defensin) proteins from Brassica. The DNA and protein sequences of the invention are useful for producing transformed plants with composite disease resistance, especially resistant to diseases caused by pathogenic bacteria, such as: rice white leaf blight, brown-stripe disease, glume blight, and seedling damping-off disease. As well as diseases caused by filamentous fungi, such as: rice blight, sheath blight disease, and leaf blight. The present DNA sequence encodes a Brassica defensin protein of the invention.

Sequence 394 BP; 116 A; 71 C; 82 G; 125 T; 0 U; 0 Other;



```

PF 07-JUN-2004; 2004JP-00169986.
XX
PR 18-SEP-2001; 2001JP-00283117.
XX
PR 18-SEP-2001; 2001JP-00283117.
XX
PA (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.
XX
DR WPI; 2004-809169/80.
XX
DR P-PSDB; ADU71301.
XX
PT Novel Brassica sp. derived protein having antimicrobial activity, useful
PT for producing multiple disease resistant plants.
XX
PS Example 2; SEQ ID NO 1; 16pp; Japanese.
XX
CC The invention comprises the amino acid and coding sequence of an
CC antimicrobial protein obtained from Brassica sp. The DNA and protein
CC sequences of the invention are useful in the production of a multiple
CC disease resistant plant. The present cDNA sequence encodes the Brassica
CC oleracea defensin protein.
XX
SQ Sequence 394 BP; 116 A; 71 C; 82 G; 125 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2,438-42 Length: 394
Score: 423.00 Matches: 76
Percent Similarity: 96.2% Conservative: 1
Best Local Similarity: 95.0% Mismatches: 3
Query Match: 95.9% Indels: 0
DB: 13 Gaps: 0

US-09-759-584-59 (1-80) x ADU71300 (1-394)
QY 1 MetAlaLysPheAlaSerIleIleAlaLeuPheAlaLeuValLeuPheAlaLa 20
DB 1 ATGGCTAAGTTTGTGTCATCATATGCCCTACTTTTGTGCTCTTTCCTGCT 60
QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTrp 40
DB 61 CTCGAAGCACCACCAATGTTGGAGGCACAGAAAGTTGTGGAGAGGCCAAGTGGGACATGG 120
QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60
DB 121 TCAGGAGTCTGTGGAAACAATAACCGATGCAAGATCAAGTGCATTAACCTTGAGAAAGCA 180
QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
DB 181 CGACATGGATCTTGCAACTATGTCTTCCAGCTCAAGTGTATTGTCTACTTCCCTTGT 240

RESULT 11
ID ADC51223
XX ADC51223 standard; DNA; 426 BP.
XX
AC ADC51223;
XX
DT 18-DEC-2003 (first entry)
XX
DE Brassica defensin protein coding sequence.
XX
KW antimicrobial protein; defensin; transgenic plant;
KW composite disease resistance; pathogenic bacteria;
KW rice white leaf blight; brown-stripe disease; glume blight;
KW seedling damping-off disease; filamentous fungi; rice blight;
KW sheath blight disease; leaf blight; gene; ds.
XX
OS Brassica sp.
XX
FH Key Location/Qualifiers
FT CDS 1..243
FT /*tag= a
FT /product= "Brassica defensin protein"
XX
PN JP2003088379-A.
XX

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PD 25-MAR-2003.
XX
PF 18-SEP-2001; 2001JP-00283117.
XX
PR 18-SEP-2001; 2001JP-00283117.
XX
PA (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.
XX
DR WPI; 2003-621123/59.
XX
DR P-PSDB; ADC51224.
XX
PT Novel protein from Brassica campestris, useful as antimicrobial against
PT plant pathogenic filamentous fungi or pathogenic bacteria, especially for
PT treating e.g. rice white leaf blight and sheath blight disease.
XX
PS Claim 3; SEQ ID NO 3; 34pp; Japanese.
XX
CC The invention comprises the amino acid and coding sequences of
CC antimicrobial (defensin) proteins from Brassica. The DNA and protein
CC sequences of the invention are useful for producing transformed plants
CC with composite disease resistance, especially resistant to diseases
CC caused by pathogenic bacteria, such as: rice white leaf blight, brown-
CC stripe disease, glume blight, and seedling damping-off disease. As well
CC as diseases caused by filamentous fungi, such as: rice blight, sheath
CC blight disease, and leaf blight. The present DNA sequence encodes a
CC Brassica defensin protein of the invention.
XX
SQ Sequence 426 BP; 142 A; 72 C; 84 G; 128 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1,948-41 Length: 426
Score: 416.00 Matches: 75
Percent Similarity: 95.0% Conservative: 1
Best Local Similarity: 93.8% Mismatches: 4
Query Match: 94.3% Indels: 0
DB: 10 Gaps: 0

US-09-759-584-59 (1-80) x ADC51223 (1-426)
QY 1 MetAlaLysPheAlaSerIleIleAlaLeuPheAlaLeuValLeuPheAlaLa 20
DB 1 ATGGCAAGTTTGTGCTCTATCATTTGCCACCTTTTGTCTCTTCTTTTAGCTGCT 60
QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTrp 40
DB 61 TTCGAGGACCAACCAATGTTGGAGGCACAGAAAGTTGTGGAGAGGCCAAGTGGGACATGG 120
QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60
DB 121 TCAGGAGTCTGTGGAAACAATAACCGATGCAAGATCAAGTGCATTAACCTTGAGAAAGCA 180
QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
DB 181 CGACATGGATCTTGCAACTATGTCTTCCAGCTCAAGTGTATTGTCTACTTCCCTTGT 240

RESULT 12
ADU71302
ID ADU71302 standard; DNA; 426 BP.
XX
AC ADU71302;
XX
DT 10-FEB-2005 (first entry)
XX
DE Brassica antimicrobial protein coding sequence - SEQ ID 3.
XX
KW antimicrobial; plant disease resistance; gene; ds.
XX
OS Brassica sp.
XX
FH Key Location/Qualifiers
FT CDS 1..243
FT /*tag= a
FT /product= "Brassica antimicrobial protein - SEQ ID 4"
XX

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```

XX JP2004329215-A.
PN
XX
XX
XX PD
XX
XX
XX PF
XX
XX PF
XX
XX PR
XX
XX PA
XX
XX PA
XX
XX DR
XX
XX DR
XX
XX PT
XX
XX PT
XX
XX PS
XX
XX CC
XX
XX CC
XX
XX CC
XX
XX CC
XX
XX CC
XX
XX CC
XX
XX SQ
Sequence 426 BP; 142 A; 72 C; 84 G; 128 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.94e-41 Length: 426
Score: 416.00 Matches: 75
Percent Similarity: 95.0% Conservative: 1
Best Local Similarity: 93.8% Mismatches: 4
Query Match: 94.3% Indels: 0
DB: 13 Gaps: 0

US-09-759-584-59 (1-80) x ADU71302 (1-426)
QY 1 MetAlaLysPheAlaSerIleIleAlaLeuPheAlaAlaLeuValLeuPheAlaAla 20
DB 1 ATGGCCAAAGTTTGTGTCATCATGTGCCCACTTTTGTGCTCTTGTCTTTTAGCTGCT 60
QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTrp 40
DB 61 TTCAGGCGCCACCATGTGGAGGACACAGAACTTGTGGAGAGGCCAAGTGGGACATGG 120
QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60
DB 121 TCAGGAGTCTGTGGAAACAATAACGCATGCATGCAAGATCAGTGCAATTAACCTTGAGAAAGCA 180
QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
DB 181 CGACATGGATCTTGCACACTATGTCTTCCAGCTCACAGGTATTTGCTACTTCCCTTGT 240

RESULT 13
ABQ82690
ID ABQ82690 standard; cDNA; 243 BP.
XX
XX AC
XX ABQ82690;
XX
XX DT
XX 02-JAN-2003 (first entry)
XX
XX DE
XX Wasabia japonica gamma-thionin encoding cDNA SEQ ID NO:1.
XX
XX KW
XX Wasabia japonica; gamma-thionin; plant; disease-resistant plant; gene;
XX
XX KW
XX ss.
XX
XX OS
XX Eutrema wasabi.
XX
XX FH
XX Key Location/Qualifiers
XX CDS 1..243
XX FT /*tag= a
XX FT /product= "gamma-thionin"
XX

```

```

PN JP2002272292-A.
XX
XX PD
XX
XX 24-SEP-2002.
XX
XX PF
XX 22-MAR-2001; 2001JP-00083526.
XX
XX PR
XX 22-MAR-2001; 2001JP-00083526.
XX
XX PA
XX (IWAT-) IWATE KEN.
XX
XX DR
XX WPI; 2002-718704/78.
XX
XX DR
XX P-PSDB; ABP53725.
XX
XX PT
XX A disease-resistant plant in which wasabi gamma-thionin gene is
XX introduced, creation of the disease-resistant plant.
XX
XX PS
XX Claim 3; Page 8; 11pp; Japanese.
XX
XX CC
XX The present invention describes a disease-resistant plant in which a
XX wasabi gamma-thionin gene is introduced. Also described is a method for
XX the creation of the above disease-resistant plant by introducing a wasabi
XX gamma-thionin gene to a plant. The present sequence encodes a Eutrema
XX wasabi (Wasabia japonica) gamma-thionin protein from the present
XX invention
XX
XX SQ
Sequence 243 BP; 60 A; 54 C; 55 G; 74 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.46e-39 Length: 243
Score: 398.00 Matches: 70
Percent Similarity: 95.0% Conservative: 6
Best Local Similarity: 87.5% Mismatches: 4
Query Match: 90.2% Indels: 0
DB: 6 Gaps: 0

US-09-759-584-59 (1-80) x ABQ82690 (1-243)
QY 1 MetAlaLysPheAlaSerIleIleAlaLeuPheAlaAlaLeuValLeuPheAlaAla 20
DB 1 ATGGCTAAGTTTGTCTTCTATCATGCTCTTCTTCGCTGCTTCTTCTTTCTTTCTGCT 60
QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTrp 40
DB 61 TTTGAAGCACCATCAATGGTGGAGCGCAGAAAGTTGTGGAGAGTCAAGTGGGACATGG 120
QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60
DB 121 TCAGGAGTCTGTGGAAACAACAACATGGTGGTCAAGAAATCAGTGCAATCAACCTTGAGGAGCA 180
QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
DB 181 CGACATGGATCTTGCACACTATATCTTCCATATCAGATGATCTGTACTTCCCATGT 240

RESULT 14
AAZ39123
ID AAZ39123 standard; cDNA to mRNA; 414 BP.
XX
XX AC
XX AAZ39123;
XX
XX DT
XX 15-SEP-2003 (revised)
XX
XX DT
XX 01-MAR-2000 (first entry)
XX
XX DE
XX Wasabia japonica antibacterial protein encoding cDNA SEQ ID NO:1.
XX
XX KW
XX Wasabia japonica; antibacterial; food additive; ds.
XX
XX OS
XX Eutrema wasabi.
XX
XX FH
XX Key Location/Qualifiers
XX CDS 1..243
XX FT /*tag= a
XX FT /product= "antibacterial protein"
XX

```

```
PN JP11313678-A.
XX
XX 16-NOV-1999.
XX
XX 30-APR-1998; 98JP-00121303.
XX
XX 30-APR-1998; 98JP-00121303.
XX
XX (IWAT-) IWATE KEN.
XX
XX WPI; 2000-057353/05.
XX
XX P-PSDB; AAY57564.
XX
XX
XX An antibacterial protein gene of Wasabia japonica - useful as a food- or
PT feed-additive.
XX
XX Claim 3; Page 12-13; 16pp; Japanese.
XX
XX The present sequence encodes an antibacterial protein isolated from
CC Wasabia japonica. The antibacterial protein can be used as a food or feed
CC additive. (Updated on 15-SEP-2003 to standardise OS field)
XX
XX Sequence 414 BP; 108 A; 79 C; 80 G; 147 T; 0 U; 0 Other;
SQ
Alignment Scores:
Pred. No.: 2.98e-39 Length: 414
Score: 398.00 Matches: 70
Percent Similarity: 95.0% Conservative: 6
Best Local Similarity: 87.5% Mismatches: 4
Query Match: 90.2% Indels: 0
DB: 3 Gaps: 0
US-09-759-584-59 (1-80) x AAZ39123 (1-414)
QY 1 MetAlaLysPheAlaSerIleAlaLeuLeuPheAlaLeuValLeuPheAlaAla 20
DB 1 ATGGCTAAGTTTGGCTTCTATCATCGCTCTTCTTCGCTGCTTGTCTTCTTCTGCT 60
QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTrp 40
DB 61 TTTGAAGCACCACCAATCGTGGAGCGCAGAGAGTTGTGGAGAGTCAAGTGGGACATGG 120
QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60
DB 121 TCAGGAGTGTGGAAACAACCAATCGTGGAGAGATCAAGTCAACCTTGAGGGAGCA 180
QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
DB 181 CGACATGGATCTTGCACATATATCTTCCATATATCAGATGATCTGTACTTCCCATGT 240
RESULT 15
ID ABZ14241
XX ABZ14241 standard; DNA; 243 BP.
XX
XX ABZ14241;
XX
XX 21-JAN-2003 (first entry)
XX
XX Arabidopsis thaliana stress regulated gene SEQ ID NO 2046.
XX
XX Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
XX
XX Arabidopsis thaliana.
XX
XX WO200216655-A2.
XX
XX 28-FEB-2002.
XX
XX 24-AUG-2001; 2001WO-05026685.
XX
XX 24-AUG-2000; 2000US-0227866P.
XX
XX 26-JAN-2001; 2001US-0264647P.
XX
XX 22-JUN-2001; 2001US-0300111P.
XX
XX (SCRI ) SCRIPES RES INST.
XX (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX
XX Harper JP, Kreps J, Wang X, Zhu T;
XX
XX WPI; 2002-304127/34.
XX
XX Identifying a stress condition to which a plant cell has been exposed and
PT producing plants with increased tolerance to these abiotic stresses.
XX
XX Claim 144; SEQ ID NO 2046; 577pp + Sequence Listing; English.
XX
XX The invention relates to identifying a stress condition to which a plant
CC cell has been exposed, comprising: (a) contacting nucleic acid
CC representative of expressed polynucleotides in the plant cell with an
CC array or probes representative of the plant cell genome; and (b)
CC detecting a profile of expressed polynucleotides in the plant cell
CC characteristic of a stress response. The method is useful in the
CC production of transgenic plants, cells and seeds and in producing plants
CC with increased tolerance to abiotic stress. The present sequence is that
CC of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used
CC in methods of the invention. Note: The sequence data for this patent is
CC not represented in the printed specification but is based on sequence
CC information supplied to Derwent by the European Patent Office
XX
XX Sequence 243 BP; 62 A; 57 C; 58 G; 66 T; 0 U; 0 Other;
SQ
Alignment Scores:
Pred. No.: 4.5e-39 Length: 243
Score: 394.00 Matches: 69
Percent Similarity: 93.8% Conservative: 6
Best Local Similarity: 86.2% Mismatches: 5
Query Match: 89.3% Indels: 0
DB: 6 Gaps: 0
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DB 1 ATGGCTAAGTTTGGCTTCTATCATCACCTTATCTTCGCTGCTTGTCTTCTTGTCTGCT 60
QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTrp 40
DB 61 TTCGACGCGCCGCAATCGTGGAGCAGACAGAAAGTTGTGGAGAGCCCAAGTGGGACATGG 120
QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60
DB 121 TCAGGGGTTTGGCGAAACAGTAATGATGCAAGATCATGTCAGTGCATTAACTTGAAGAGCC 180
QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
DB 181 AACATGATCATGCAACTATGCTTCTCCAGCAGACACAGATGATCTGTATGCTCCCATGT 240
Search completed: May 10, 2006, 06:01:44
Job time : 455 secs
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GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: May 10, 2006, 06:02:00 ; Search time 3003.5 Seconds  
(without alignments)  
1869.302 Million cell updates/sec

Title: US-09-759-584-59  
Perfect score: 441  
Sequence: 1 MAKFAIIALLFAALVLFPA.....RHGSCNYVPPAHKCIYPPC 80

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
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-Q=/abs/ABSSWEB spool/US09759584/runat\_08052006\_175231\_11286/app\_query.fasta\_1  
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-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abs03h  
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1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_est3:\*  
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11: gb\_gss3:\*

Result No. Score Match Length DB ID Description

1	432	98.0	425	6	CD834852	CD834852 BN45.043G08F011229 BN45 Brassica napus cdna clone BN45043G08, mRNA
2	432	98.0	427	6	CD833613	CD833613 BN40.067P
3	432	98.0	449	6	CD833047	CD833047 BN40.065M
4	432	98.0	523	6	CD833661	CD833661 BN45.001C
5	432	98.0	543	6	CD828840	CD828840 BN40.040A
6	428	97.1	522	6	CD833938	CD833938 BN45.040A
7	428	97.1	646	6	CD829429	CD829429 BN40.042B

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	432	98.0	425	6	CD834852	CD834852 BN45.043G
2	432	98.0	427	6	CD833613	CD833613 BN40.067P
3	432	98.0	449	6	CD833047	CD833047 BN40.065M
4	432	98.0	523	6	CD833661	CD833661 BN45.001C
5	432	98.0	543	6	CD828840	CD828840 BN40.040A
6	428	97.1	522	6	CD833938	CD833938 BN45.040A
7	428	97.1	646	6	CD829429	CD829429 BN40.042B

8	427	96.8	413	7	CD826227	CD826227 EL1386 Bx
9	427	96.8	418	6	CD832825	CD832825 BN40.064A
10	427	96.8	420	6	CD833944	CD833944 BN45.040B
11	427	96.8	421	6	CD826491	CD826491 BN25.064A
12	427	96.8	421	6	CD831111	CD831111 BN40.058A
13	427	96.8	421	6	CD833977	CD833977 BN45.040D
14	427	96.8	422	6	CD833983	CD833983 BN45.040D
15	427	96.8	426	6	CD827413	CD827413 BN25.067G
16	427	96.8	438	6	CD831294	CD831294 BN40.058N
17	427	96.8	438	6	CD831479	CD831479 BN40.059J
18	427	96.8	453	6	CD834008	CD834008 BN45.040E
19	427	96.8	453	7	CD826424	CD826424 3ETMS UP
20	427	96.8	456	7	CD826661	CD826661 3ETMS UP
21	427	96.8	480	6	CD828332	CD828332 BN25.070H
22	427	96.8	553	6	CD831014	CD831014 BN40.047K
23	426	96.6	376	7	CD827135	CD827135 EL2049F B
24	426	96.6	408	6	CD833779	CD833779 BN45.001I
25	426	96.6	409	6	CD832294	CD832294 BN40.062L
26	426	96.6	409	6	CD834090	CD834090 BN45.040I
27	426	96.6	446	6	CD834068	CD834068 BN45.040H
28	426	96.6	447	6	CD832592	CD832592 BN40.063O
29	426	96.6	450	6	CD834611	CD834611 BN45.042H
30	426	96.6	452	6	CD832071	CD832071 BN40.061O
31	426	96.6	458	6	CD834994	CD834994 BN45.043O
32	426	96.6	458	7	CD827136	CD827136 EL2049R B
33	426	96.6	470	6	CD831680	CD831680 BN40.060H
34	426	96.6	473	6	CD834995	CD834995 BN45.043O
35	426	96.6	481	6	CD833924	CD833924 BN45.040A
36	426	96.6	482	6	CD833627	CD833627 BN45.001A
37	426	96.6	484	7	CD826241	CD826241 3ETMS UP
38	426	96.6	485	7	CD826374	CD826374 3ETMS UP
39	426	96.6	547	7	CD826625	CD826625 3ETMS UP
40	426	96.6	566	7	CD825823	CD825823 17ACDHMS
41	426	96.6	592	7	CD826094	CD826094 17ACDHMS
42	426	96.6	597	7	CD826329	CD826329 3ETMS UP
43	424	96.1	419	6	CD834168	CD834168 BN45.040N
44	423	95.9	543	6	CD830628	CD830628 BN40.046D
45	422	95.7	458	7	CD826701	CD826701 3ETMS UP

ALIGNMENTS

RESULT 1  
CD834852  
LOCUS BN45.043G08F011229 BN45 Brassica napus cdna clone BN45043G08, mRNA  
DEFINITION linear EST 10-JUL-2003  
ACCESSION CD834852  
VERSION CD834852.1 GI:32516792  
KEYWORDS sequence.  
SOURCE EST.  
ORGANISM Brassica napus (rape)  
Brassica napus  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
REFERENCE 1 (bases 1 to 425)  
AUTHORS Genoplante.  
TITLE Genoplante, a major partnership french program in plant genomics  
JOURNAL Unpublished (2003)  
COMMENT Contact: Genoplante  
Genoplante  
93, rue Henri Rochefort 91025 EVRY CEDEX France  
Tel: 33 1 69 47 54 00  
Fax: 33 1 69 47 54 10  
This sequence has been generated in the framework of the french  
plant genomics programme 'Genoplante' (<http://www.genoplante.com>  
and <http://genoplante-info.infobloggen.fr>).  
FEATURES  
source  
1..425  
/organism="Brassica napus"  
/mol\_type="mRNA"  
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/db\_xref="taxon:3708"

/clone="BN45043G08"  
/tissue\_type="seed"  
/clone\_lib="BN45"

## ORIGIN

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Pred. No.: 1.14e-40 Length: 425  
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Best Local Similarity: 95.0% Mismatches: 0  
Query Match: 98.0% Indels: 0  
DB: 6 Gaps: 0

US-09-759-584-59 (1-80) x CD834852 (1-425)

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DB 49 ATGGCTAAGTTTGGCTTCCATCGTTGCCCTTCTTTCTGCGCTTGTATTTTGTGCT 108  
QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTtp 40  
DB 109 TTCGAAGCACCACAAATGTTGGGAAGCACAGAAGCTGTGCAAGGCCAAGTGAACGTGG 168  
QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60  
DB 169 TCAGGAGTCTGTGGAAACAATAATGATGCAAGAATCAGTGCATTGCAGTAGAAGCA 228  
QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80  
DB 229 CGACATGGATCTTGCACATATGTCTTCCAGCTCACAAGTGCATCTGCTACTTCCCTGT 288

## RESULT 2

CD833613 427 bp mRNA linear EST 10-JUL-2003  
LOCUS BN40.067P16F011228 BN40 Brassica napus cDNA clone BN40067P16, mRNA  
DEFINITION sequence.

ACCESSION CD833613

VERSION CD833613.1 GI:32515553

KEYWORDS EST.

SOURCE Brassica napus (rape)

ORGANISM

Brassica napus  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE 1 (bases 1 to 427)

Genoplatte.

AUTHORS Genoplatte, a major partnership french program in plant genomics

TITLE Genoplatte, a major partnership french program in plant genomics

JOURNAL Unpublished (2003)

COMMENT Contact: Genoplatte

Genoplatte

93, rue Henri Rochefort 91025 EVRY CEDEX France

Tel: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french  
plant genomics programme 'Genoplatte' (<http://www.genoplatte.com>  
and <http://genoplatte-info.infobiogen.fr>).

## FEATURES

source  
Location/Qualifiers  
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/organism="Brassica napus"  
/mol\_type="mRNA"  
/cultivar="Jet Neuf"  
/db\_xref="taxon:3708"  
/clone="BN40067P16"  
/tissue\_type="seed"  
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## ORIGIN

## Alignment Scores:

Pred. No.: 1.15e-40 Length: 427  
Score: 432.00 Matches: 76  
Percent Similarity: 100.0% Conservative: 4  
Best Local Similarity: 95.0% Mismatches: 0  
Query Match: 98.0% Indels: 0

DB: 6 Gaps: 0  
US-09-759-584-59 (1-80) x CD833613 (1-427)

QY 1 MetAlaLysPheAlaSerIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 20  
DB 51 ATGGCTAAGTTTGGCTTCCATCGTTGCCCTTCTTTCTGCGCTTGTATTTTGTGCTGT 110  
QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTtp 40  
DB 111 TTCGAAGCACCACAAATGTTGGGAAGCACAGAAGCTGTGCAAGGCCAAGTGAACGTGG 170  
QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60  
DB 171 TCAGGAGTCTGTGGAAACAATAATGATGCAAGAATCAGTGCATTGCAGTAGAAGCA 230  
QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80  
DB 231 CGACATGGATCTTGCACATATGTCTTCCAGCTCACAAGTGCATCTGCTACTTCCCTGT 290

## RESULT 3

CD833047

LOCUS

DEFINITION

ACCESSION CD833047

VERSION CD833047.1

KEYWORDS EST.

SOURCE Brassica napus (rape)

ORGANISM

Brassica napus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE 1 (bases 1 to 449)

Genoplatte.

AUTHORS Genoplatte, a major partnership french program in plant genomics

TITLE Genoplatte, a major partnership french program in plant genomics

JOURNAL Unpublished (2003)

COMMENT Contact: Genoplatte

Genoplatte

93, rue Henri Rochefort 91025 EVRY CEDEX France

Tel: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french  
plant genomics programme 'Genoplatte' (<http://www.genoplatte.com>  
and <http://genoplatte-info.infobiogen.fr>).

## FEATURES

source  
Location/Qualifiers  
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/mol\_type="mRNA"  
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/clone="BN40065M05"  
/tissue\_type="seed"  
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## ORIGIN

Alignment Scores:  
Pred. No.: 1.22e-40 Length: 449  
Score: 432.00 Matches: 76  
Percent Similarity: 100.0% Conservative: 4  
Best Local Similarity: 95.0% Mismatches: 0  
Query Match: 98.0% Indels: 0  
DB: 6 Gaps: 0

US-09-759-584-59 (1-80) x CD833047 (1-449)

QY 1 MetAlaLysPheAlaSerIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 20  
DB 32 ATGGCTAAGTTTGGCTTCCATCGTTGCCCTTCTTTCTGCGCTTGTATTTTGTGCTGT 91  
QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTtp 40  
DB 92 TTCGAAGCACCACAAATGTTGGGAAGCACAGAAGCTGTGCAAGGCCAAGTGAACGTGG 151

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Db 152 TCAGGAGTCTGTGGAACAATAATGTCATCAAGAAATCAGTGCATTCGACTAGAGAAGCA 211
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|
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QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
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Db 212 CGACATGGATCTTGCAACTATGTCTTCCAGCTCAAGTGCATCTGTCTACTTCCCTTGT 271
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RESULT 4
CD833661
LOCUS
DEFINITION
BN45.001C04F010914 BN45 Brassica napus cDNA clone BN45001C04, mRNA
sequence.
ACCESSION
CD833661
VERSION
CD833661.1 GI:32515601
KEYWORDS
EST.
SOURCE
Brassica napus (rape)
ORGANISM
Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
1 (bases 1 to 523)
Genoplante.
AUTHORS
Genoplante, a major partnership french program in plant genomics
TITLE
Unpublished (2003)
JOURNAL
Contact: Genoplante
COMMENT
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com)
and http://genoplante-info.infobiogen.fr.
FEATURES
source
Location/Qualifiers
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Score: 432.00 Matches: 76
Percent Similarity: 100.0% Conservative: 4
Best Local Similarity: 95.0% Mismatches: 0
Query Match: 98.0% Indels: 0
DB: 6 Gaps: 0
US-09-759-584-59 (1-80) x CD833661 (1-523)
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Db 52 ATGGCTAAGTTGCTTCATCGTTCCTCTCTCTCTGCTGCTGTTATTTTGTCT 111
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|
QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTrp 40
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Db 112 TTCGAGGACCAACAATGTCGGAAGCACAGAGCTGTGCGAAGGCCAAGTGCACGCTGG 171
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QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAArgLeuGluLysAla 60
|
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|
Db 172 TCAGGAGTCTGTGGAACAATAATGTCATCAAGAAATCAGTGCATTCGACTAGAGAAGCA 231
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QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
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Db 232 CGACATGGATCTTGCAACTATGTCTTCCAGCTCAAGTGCATCTGTCTACTTCCCTTGT 291
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RESULT 5
CD828840
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LOCUS
DEFINITION
CD828840 543 bp mRNA linear EST 10-JUL-2003
BN40.040A23F011019 BN40 Brassica napus cDNA clone BN40040A23, mRNA
sequence.
ACCESSION
CD828840
VERSION
CD828840.1 GI:32510780
KEYWORDS
EST.
SOURCE
Brassica napus (rape)
ORGANISM
Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
1 (bases 1 to 543)
Genoplante.
AUTHORS
Genoplante, a major partnership french program in plant genomics
TITLE
Unpublished (2003)
JOURNAL
Contact: Genoplante
COMMENT
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com)
and http://genoplante-info.infobiogen.fr.
FEATURES
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/tissue_type="seed"
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Score: 432.00 Matches: 76
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Query Match: 98.0% Indels: 0
DB: 6 Gaps: 0
US-09-759-584-59 (1-80) x CD828840 (1-543)
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|
|
Db 111 TTCGAGGACCAACAATGTCGGAAGCACAGAGCTGTGCGAAGGCCAAGTGCACGCTGG 170
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QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAArgLeuGluLysAla 60
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|
|
Db 171 TCAGGAGTCTGTGGAACAATAATGTCATCAAGAAATCAGTGCATTCGACTAGAGAAGCA 230
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|
|
QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
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|
|
Db 231 CGACATGGATCTTGCAACTATGTCTTCCAGCTCAAGTGCATCTGTCTACTTCCCTTGT 290
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|
|
RESULT 6
CD833938
LOCUS
DEFINITION
BN45.040A23F011018 BN45 Brassica napus cDNA clone BN45040A23, mRNA
sequence.
ACCESSION
CD833938
VERSION
CD833938.1 GI:32515878
KEYWORDS
EST.
SOURCE
Brassica napus (rape)
ORGANISM
Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
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REFERENCE 1 (bases 1 to 522)  
 AUTHORS Genoplante.  
 TITLE Genoplante, a major partnership french program in plant genomics  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Genoplante  
 Genoplante  
 93, rue Henri Rochefort 91025 EVRY CEDEX France  
 Tel: 33 1 69 47 54 00  
 Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (<http://www.genoplante.com>) and <http://genoplante-info.infobiogen.fr>.

## FEATURES

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Location/Qualifiers  
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 Percent Similarity: 100.0% Conservative: 5  
 Best Local Similarity: 93.8% Mismatches: 0  
 Query Match: 97.1% Indels: 0  
 DB: 6 Gaps: 0

US-09-759-584-59 (1-80) x CD833938 (1-522)

QY 1 MetAlaLyPheAlaSerIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 20  
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 Db 51 ATGGCTAAGTTGCTTCCATCGTTGCCCTTCTTTCTCTGCCCCTGTTATTGTTGCT 110  
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 QY 21 PheGluAlaProThrMetValGluAlaGlnLyLeuCysGlnArgProSerGlyThrTTP 40  
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 Db 111 TTGGAAGCACCACAAATGGTGGGAAGCAGACAGCTGTGCGAAGGCCAAGTGGACGTGG 170  
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 QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60  
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 Db 171 TCAGGAGTCTGTGGAACCAATATGATGCATGCAAGATCAGTGCATTCGACTAAGAAGCA 230  
 |||||  
 QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80  
 |||||  
 Db 231 CGACATGGATCTTGCAACTATGTCTCCAGCTCACAAGTGCACTGCTACTTCCCTTGT 290  
 |||||

RESULT 7  
 CD829429  
 LOCUS BN40.042B06F011226 BN40 Brassica napus cDNA clone BN40042B06, mRNA  
 DEFINITION sequence.  
 EST. CD829429.1 GI:32511369

ACCESSION CD829429  
 VERSION CD829429.1  
 KEYWORDS EST.  
 SOURCE Brassica napus (rape)  
 ORGANISM Brassica napus  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
 1 (bases 1 to 646)

REFERENCE Genoplante.  
 AUTHORS Genoplante.  
 TITLE Genoplante, a major partnership french program in plant genomics  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Genoplante  
 Genoplante  
 93, rue Henri Rochefort 91025 EVRY CEDEX France  
 Tel: 33 1 69 47 54 00  
 Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (<http://www.genoplante.com>)

and <http://genoplante-info.infobiogen.fr>.

## FEATURES

source

Location/Qualifiers  
 1..646  
 /organism="Brassica napus"  
 /mol\_type="mRNA"  
 /cultivar="Jet Neuf"  
 /db\_xref="taxon:3708"  
 /clone="BN40042B06"  
 /issue\_type="seed"  
 /clone\_lib="BN40"

## ORIGIN

Alignment Scores:  
 Pred. No.: 5,85e-40 Length: 646  
 Score: 428.00 Matches: 75  
 Percent Similarity: 98.8% Conservative: 4  
 Best Local Similarity: 93.8% Mismatches: 1  
 Query Match: 97.1% Indels: 0  
 DB: 6 Gaps: 0

US-09-759-584-59 (1-80) x CD829429 (1-646)

QY 1 MetAlaLyPheAlaSerIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 20  
 |||||  
 Db 45 ATGGCTAAGTTGCTTCCATCGTTGCCCTTCTTTCTCTGCCCCTGTTATTGTTGCT 104  
 |||||  
 QY 21 PheGluAlaProThrMetValGluAlaGlnLyLeuCysGlnArgProSerGlyThrTTP 40  
 |||||  
 Db 105 TTGGAAGCACCACAAATGGTGGGAAGCAGACAGCTGTGCGAAGGCCAAGTGGACGTGG 164  
 |||||  
 QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60  
 |||||  
 Db 165 TCAGGAGTCTGTGGAACCAATATGATGCATGCAAGATCAGTGCATTCGACTAAGAAGCA 224  
 |||||  
 QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80  
 |||||  
 Db 225 CGCATGGATCTTGCAACTATGTCTCCAGCTCACAAGTGCACTGCTACTTCCCTTGT 284  
 |||||

## RESULT 8

CDN826227

LOCUS

DEFINITION

ELI386 Brassica embryo library (EL) Brassica napus cDNA clone

ELI386 complete, mRNA sequence.

ACCESSION

CN826227

VERSION

CN826227.1

KEYWORDS

EST.

SOURCE

Brassica napus (rape)

ORGANISM

Brassica napus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
1 (bases 1 to 413)

REFERENCE

AUTHORS

TITLE

Brassica napus ESTs

JOURNAL

Unpublished (2004)

COMMENT

Contact: Sharpe, A.G.  
Molecular Genetics  
Agriculture & Agri-Food Canada  
107 Science Place, Saskatoon, Saskatchewan, Canada, S7N0X2  
Tel: 306 956 7271  
Fax: 306 956 7247  
Email: sharpea@agr.gc.ca  
Seq primer: M13 Forward and T7.  
Location/Qualifiers  
1..413  
/organism="Brassica napus"  
/mol\_type="mRNA"  
/cultivar="DH12075 (double haploid line from Cresor x  
Westar cross)"  
/db\_xref="taxon:3708"  
/clone="ELI386"  
/dev\_stage="Mid to late embryos (4-6 mg)"  
/lab\_host="E. coli Electromax DH5 alpha-e (Invitrogen)"



/clone lib="Brassica embryo library (EL)"  
 /notes="Organ: Embryos without seed coat; Vector: pSPOR1  
 (modified: GCGCGCCG\*GACTAGTACGTC\*cgagcgtgggtcgac);  
 Site 1: Noti; Site 2: Sali; Seeds were collected by Dr.  
 Francois Ouellet when they were still very green (mid to  
 large stage, cotyledons were formed). The seed coats were  
 removed and the remaining tissue was used for cDNA library  
 construction. mRNA was poly-A primed using Superscript  
 Plasmid System cDNA Synthesis and Cloning kit (Invitrogen)  
 After initial screening, the most abundant redundant  
 clones were screened out using 22 oligos designed to match  
 napins (including albumins), cruciferins, oleosins, HSP70,  
 trypsin inhibitor 2, cytosolic GAPDH, cyclophilins, HSP70,  
 desaturase, and CAB (LHCP)."

## ORIGIN

Alignment Scores:  
 Pred. No.: 4,26e-40 Length: 413  
 Score: 427.00 Matches: 77  
 Percent Similarity: 97.5% Conservative: 1  
 Best Local Similarity: 96.2% Mismatches: 2  
 Query Match: 96.8% Indels: 0  
 DB: 7 Gaps: 0

US-09-759-584-59 (1-80) x CN826227 (1-413)

QY 1 MetAlaLysPheAlaSerIleAlaLeuLeuPheAlaLeuValLeuPheAlaA 20  
 |||||  
 Db 28 ATGGCTAAGTTGCTTCCATCATTTGCTCTTTTGTCTCTTTTGTCTCT 87  
 |||||  
 QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTyr 40  
 |||||  
 Db 88 CTCGAAGCACCACCAATGCTGGAAGCACAGAAGTTGTGCGAGAGGCCAAGTGGGACATGG 147  
 |||||  
 QY 41 SerGlyValCysGlyValAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60  
 |||||  
 Db 148 TCAGAGTCTGTGGAACCAATTAACGATCAGATCAAGATCAATTAACCTTGAGAAGCA 207  
 |||||  
 QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80  
 |||||  
 Db 208 CGACATGGATCTTGCACATATGCTTCCAGCTCACAGTGTATTGCTACTTCCCTTGT 267  
 |||||

RESULT 9  
 CD832625  
 LOCUS BN40.064A14F011227 BN40 Brassica napus cDNA clone BN40064A14, mRNA  
 DEFINITION  
 sequence.  
 CD832625  
 ACCESSION  
 VERSION CD832625.1 GI:32514565  
 KEYWORDS EST.  
 SOURCE Brassica napus (rape)  
 ORGANISM Brassica napus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
 1 (bases 1 to 418)  
 Genoplatante.  
 Genoplatante, a major partnership french program in plant genomics  
 Unpublished (2003)  
 Contact: Genoplatante  
 Genoplatante  
 93, rue Henri Rochefort 91025 EVRY CEDEX France  
 Tel: 33 1 69 47 54 00  
 Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french  
 plant genomics programme 'Genoplatante' (<http://www.genoplatante.com>  
 and <http://genoplatante-info.infobiogen.fr>).  
 Location/Qualifiers  
 1..418  
 /organism="Brassica napus"  
 /mol\_type="mRNA"  
 /cultivar="Jet Neuf"  
 /db\_xref="taxon:3708"

## FEATURES

source  
 Alignment Scores:  
 Pred. No.: 4.36e-40 Length: 420  
 Score: 427.00 Matches: 77  
 Percent Similarity: 97.5% Conservative: 1  
 Best Local Similarity: 96.2% Mismatches: 2  
 Query Match: 96.8% Indels: 0

/clone="BN40064A14"  
 /tissue\_type="seed"  
 /clone\_lib="BN40"

## ORIGIN

Alignment Scores:  
 Pred. No.: 4,33e-40 Length: 418  
 Score: 427.00 Matches: 77  
 Percent Similarity: 97.5% Conservative: 1  
 Best Local Similarity: 96.2% Mismatches: 2  
 Query Match: 96.8% Indels: 0  
 DB: 6 Gaps: 0

US-09-759-584-59 (1-80) x CD832625 (1-418)

QY 1 MetAlaLysPheAlaSerIleAlaLeuLeuPheAlaLeuValLeuPheAlaA 20  
 |||||  
 Db 53 ATGGCAAGTTGCTTCCATCATTTGCTCTTTTGTCTCTTTTGTCTCT 112  
 |||||  
 QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTyr 40  
 |||||  
 Db 113 CTCGAAGCACCACCAATGCTGGAAGCACAGAAGTTGTGCGAGAGGCCAAGTGGGACATGG 172  
 |||||  
 QY 41 SerGlyValCysGlyValAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60  
 |||||  
 Db 173 TCAGAGTCTGTGGAACCAATTAACGATCAGATCAAGATCAATTAACCTTGAGAAGCA 232  
 |||||  
 QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80  
 |||||  
 Db 233 CGACATGGATCTTGCACATATGCTTCCAGCTCACAGTGTATTGCTACTTCCCTTGT 292  
 |||||

RESULT 10  
 CD833944

LOCUS BN45.040B07F011019 BN45 Brassica napus cDNA clone BN45040B07, mRNA  
 DEFINITION  
 sequence.  
 CD833944  
 ACCESSION  
 VERSION CD833944.1 GI:32515884  
 KEYWORDS EST.  
 SOURCE Brassica napus (rape)  
 ORGANISM Brassica napus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
 1 (bases 1 to 420)  
 Genoplatante.  
 Genoplatante, a major partnership french program in plant genomics  
 Unpublished (2003)  
 Contact: Genoplatante  
 Genoplatante  
 93, rue Henri Rochefort 91025 EVRY CEDEX France  
 Tel: 33 1 69 47 54 00  
 Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french  
 plant genomics programme 'Genoplatante' (<http://www.genoplatante.com>  
 and <http://genoplatante-info.infobiogen.fr>).  
 Location/Qualifiers  
 1..420  
 /organism="Brassica napus"  
 /mol\_type="mRNA"  
 /cultivar="Jet Neuf"  
 /db\_xref="taxon:3708"  
 /clone="BN45040B07"  
 /tissue\_type="seed"  
 /clone\_lib="BN45"

## FEATURES

source

Alignment Scores:  
 Pred. No.: 4.36e-40 Length: 420  
 Score: 427.00 Matches: 77  
 Percent Similarity: 97.5% Conservative: 1  
 Best Local Similarity: 96.2% Mismatches: 2  
 Query Match: 96.8% Indels: 0



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LOCUS
DEFINITION CD833977 421 bp mRNA linear EST 10-JUL-2003
            BN45.040D05F011019 BN45 Brassica napus cDNA clone BN45040D05, mRNA
            sequence.
ACCESSION CD833977
VERSION CD833977.1 GI:32515917
KEYWORDS EST.
SOURCE Brassica napus (rape)
ORGANISM Brassica napus
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
          rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 421)
AUTHORS Genoplante.
TITLE Genoplante, a major partnership french program in plant genomics
JOURNAL Unpublished (2003)
COMMENT Contact: Genoplante
          93, rue Henri Rochefort 91025 EVRY CEDEX France
          Tel: 33 1 69 47 54 00
          Fax: 33 1 69 47 54 10
          This sequence has been generated in the framework of the french
          plant genomics programme 'Genoplante' (http://www.genoplante.com)
          and http://genoplante-info.infobiogen.fr.
FEATURES
source 1..421
        /organism="Brassica napus"
        /mol_type="mRNA"
        /cultivar="Jet Neuf"
        /db_xref="taxon:3708"
        /clone="BN45040D05"
        /tissue_type="seed"
        /clone_lib="BN45"
ORIGIN
Alignment Scores: 4.37e-40 Length: 421
Pred. No.: 427.00 Matches: 77
Score: 97.5% Conservative: 1
Percent Similarity: 96.2% Mismatches: 2
Best Local Similarity: 96.2% Indels: 0
Query Match: 96.8% Gaps: 0
DB: 6
US-09-759-584-59 (1-80) x CD833977 (1-421)
QY 1 MetAlaLysPheAlaSerIleIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 20
    |||||
Db 51 ATGGCTAAGTTGCTTCCATCATGTCCTACTTTTGGCTGCTCTTTCCTTTTGGTGCT 110
    |||||
QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTrp 40
    |||||
Db 111 CTCGAAGCACCACCAATGTTGGAAGCACAGAAAGTTGTGCGAGAGGCCAAGTGGGACATGG 170
    |||||
QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60
    |||||
Db 171 TCAGGAGTCTGTGGAACAATAACCGCATGCAAGATCAGTGCATTAACCTTGGAAGAAGCA 230
    |||||
QY 61 AtgHieGlySerCysAsnTrValPheProAlaHisLysCysIleCysTrPheProCys 80
    |||||
Db 231 CGACATGGATCTTGGCAACTATGCTTCCAGCTCACAGTGATTTTGTACTTCCCTTGT 290
    |||||
RESULT 14
CD833983
LOCUS
DEFINITION CD833983 422 bp mRNA linear EST 10-JUL-2003
            BN45.040D11F011019 BN45 Brassica napus cDNA clone BN45040D11, mRNA
            sequence.
ACCESSION CD833983
VERSION CD833983.1 GI:32515923
KEYWORDS EST.
SOURCE Brassica napus (rape)
ORGANISM Brassica napus
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
          rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 422)
AUTHORS Genoplante.
TITLE Genoplante, a major partnership french program in plant genomics
JOURNAL Unpublished (2003)
COMMENT Contact: Genoplante
          93, rue Henri Rochefort 91025 EVRY CEDEX France
          Tel: 33 1 69 47 54 00
          Fax: 33 1 69 47 54 10
          This sequence has been generated in the framework of the french
          plant genomics programme 'Genoplante' (http://www.genoplante.com)
          and http://genoplante-info.infobiogen.fr.
FEATURES
source 1..422
        /organism="Brassica napus"
        /mol_type="mRNA"
        /cultivar="Jet Neuf"
        /db_xref="taxon:3708"
        /clone="BN45040D11"
        /tissue_type="seed"
        /clone_lib="BN45"
ORIGIN
Alignment Scores: 4.39e-40 Length: 422
Pred. No.: 427.00 Matches: 77
Score: 97.5% Conservative: 1
Percent Similarity: 96.2% Mismatches: 2
Best Local Similarity: 96.2% Indels: 0
Query Match: 96.8% Gaps: 0
DB: 6
US-09-759-584-59 (1-80) x CD833983 (1-422)
QY 1 MetAlaLysPheAlaSerIleIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 20
    |||||
Db 51 ATGGCTAAGTTGCTTCCATCATGTCCTACTTTTGGCTGCTCTTTCCTTTTGGTGCT 110
    |||||
QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTrp 40
    |||||
Db 111 CTCGAAGCACCACCAATGTTGGAAGCACAGAAAGTTGTGCGAGAGGCCAAGTGGGACATGG 170
    |||||
QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60
    |||||
Db 171 TCAGGAGTCTGTGGAACAATAACCGCATGCAAGATCAGTGCATTAACCTTGGAAGAAGCA 230
    |||||
QY 61 AtgHieGlySerCysAsnTrValPheProAlaHisLysCysIleCysTrPheProCys 80
    |||||
Db 231 CGACATGGATCTTGGCAACTATGCTTCCAGCTCACAGTGATTTTGTACTTCCCTTGT 290
    |||||
RESULT 15
CD827413
LOCUS
DEFINITION CD827413 426 bp mRNA linear EST 10-JUL-2003
            BN25.067G02F020123 BN25 Brassica napus cDNA clone BN25067G02, mRNA
            sequence.
ACCESSION CD827413
VERSION CD827413.1 GI:32509353
KEYWORDS EST.
SOURCE Brassica napus (rape)
ORGANISM Brassica napus
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
          rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 426)
AUTHORS Genoplante.
TITLE Genoplante, a major partnership french program in plant genomics
JOURNAL Unpublished (2003)
COMMENT Contact: Genoplante
          93, rue Henri Rochefort 91025 EVRY CEDEX France
          Tel: 33 1 69 47 54 00
          Fax: 33 1 69 47 54 10
          This sequence has been generated in the framework of the french
          plant genomics programme 'Genoplante' (http://www.genoplante.com)
          and http://genoplante-info.infobiogen.fr.
```

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and http://genoplante-info.infobiogen.fr).
FEATURES
  source              1..426
    Location/Qualifiers
      /organism="Brassica napus"
      /mol_type="mRNA"
      /cultivar="Jet Neuf"
      /db_xref="taxon:3708"
      /clone="BN25067G02"
      /tissue_type="seed"
      /clone_lib="BN25"

ORIGIN
Alignment Scores:
Pred. No.:      4,44e-40      Length:      426
Score:          427.00      Matches:      77
Percent Similarity: 97.5%      Conservative: 1
Best Local Similarity: 96.2%      Mismatches: 2
Query Match:     96.8%      Indels:      0
DB:              6      Gaps:      0

US-09-759-584-59 (1-80) x CD827413 (1-426)

QY      1  MetAlaLysPheAlaSerIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 20
DB      51  ATGGCTAAGTTTGCTTCCATCATTTGCTGCTCTTTGCTGCTCTTTGCTGCT 110
QY      21  PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTrp 40
DB      111  CTCGAAGCACCAACAATGGTGAAGCACAGAGTTGTGCGAGAGGCCAAGTGGGACATGG 170
QY      41  SerGlyValCysGlyAsnAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60
DB      171  TCAGGAGTCTGTGGAAACATATACGCATGCAAGATCAGTGCATTAACCTTGGAAGGCA 230
QY      61  ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
DB      231  CGACATGGATCTTGGCAACTATGTCTTCCAGCTCACAAAGTGTATTTGCTACTTCCCTTGT 290

Search completed: May 10, 2006, 09:42:56
Job time : 3006.5 secs
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GenCore version 5.1.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame plus p2n model

Run on: May 10, 2006, 05:46:44 ; Search time 3626 Seconds  
(without alignments)  
1881.195 Million cell updates/sec

Title: US-09-759-584-49  
Perfect score: 442  
Sequence: 1 MAKFASTIALLPALVFAA.....RHGSCNYVPPAHKCIYFPC 80

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+ p2n.model -DEV=xlh  
-O=/abs/ABSWEB spool/US09759584/runat\_08052006\_175228\_11238/app\_query\_fasta\_1  
-DB=GenEmbl -QFT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abes03h  
-USER=US09759584 @CNC 1.1 5142 @runat\_08052006\_175228\_11238 -NCPU=6 -ICPU=3  
-NO\_WMAP -NEG\_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG -DEV TIMEOUT=120  
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl.\*

- 1: gb.ba.\*
- 2: gb.in.\*
- 3: gb.env.\*
- 4: gb.om.\*
- 5: gb.ov.\*
- 6: gb.pat.\*
- 7: gb.ph.\*
- 8: gb.pr.\*
- 9: gb.ro.\*
- 10: gb.sts.\*
- 11: gb.sy.\*
- 12: gb.un.\*
- 13: gb.vi.\*
- 14: gb.htg.\*
- 15: gb.pl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	442	100.0	285	6	AR014692
2	442	100.0	285	6	AR432392
3	442	100.0	395	15	RSU18557

4	442	100.0	414	6	A26875
5	442	100.0	414	6	A39549
6	442	100.0	414	6	A63404
7	442	100.0	414	6	AR050153
8	442	100.0	414	6	AR130272
9	442	100.0	414	6	I23728
10	442	100.0	414	6	AR207337
11	442	100.0	414	6	AR374914
12	442	100.0	414	6	AR642703
13	433	98.0	285	6	AR014693
14	433	98.0	285	6	AR432393
15	433	98.0	288	6	A39553
16	433	98.0	288	6	AR050161
17	433	98.0	288	6	AR130280
18	433	98.0	288	6	I23736
19	423	95.7	449	6	E34290
20	418	94.6	575	6	BD223249
21	417	94.3	457	15	RSU18556
22	414	93.7	243	15	AY998243
23	407	92.1	243	6	BD174927
24	407	92.1	414	6	E31545
25	407	92.1	414	15	AB012871
26	405	91.6	499	15	RSAP94
27	403	91.2	243	6	AX412329
28	403	91.2	243	6	AX412502
29	403	91.2	243	6	AX507351
30	403	91.2	243	6	AX590057
31	403	91.2	274	15	AY133787
32	403	91.2	400	6	A68647
33	403	91.2	454	15	AY063779
34	402	91.0	243	6	BD174928
35	402	91.0	363	15	AF528180
36	402	91.0	416	6	E31546
37	402	91.0	416	15	AB012872
38	397	89.8	243	6	AX412406
39	397	89.8	243	6	AX412601
40	397	89.8	243	6	AX651878
41	397	89.8	243	15	AY060506
42	397	89.8	403	6	A68645
43	397	89.8	403	15	ATANTSPEC
44	397	89.8	425	15	AY052236
45	396.5	89.7	270	6	AR014691

ALIGNMENTS

RESULT 1	AR014692	Sequence 16 from patent US 5773696.	285 bp	DNA	linear	PAT 05-DEC-1998
LOCUS	AR014692					
DEFINITION	AR014692					
ACCESSION	AR014692					
VERSION	AR014692.1	GI:3972146				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unknown.					

REFERENCE 1 (bases 1 to 285)  
Liang, J., Shah, D. Maganlal., Wu, Y. Shun, and Rosenberger, C. Annette.  
Antifungal polypeptide and methods for controlling plant pathogenic fungi  
Patent: US 5773696-A 16 30-JUN-1998;  
Location/Qualifiers  
1..285  
/organism="unknown"  
/mol\_type="unassigned DNA"

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Pred. No.:	442.00	Matches:	80
Score:	100.0%	Conservative:	0
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Best Local Similarity:	100.0%	Indels:	0
Query Match:	100.0%		



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Db 135 TCAGGAGTCTGTGGAACCAATAACGATCGCAAGATCAAGTCAATTAACCTTGGAAGCA 194  
Qy 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80  
Db 195 CGACATGGATCTTGGCAACTATGCTTCCAGCTCACAAGTGTATCTGCTACTTTCCTTGT 254  
RESULT 4  
A26875  
LOCUS A26875 414 bp DNA linear PAT 30-NOV-2001  
DEFINITION R.sativus AFP1 gene.  
ACCESSION A26875  
VERSION A26875.1 GI:1247352  
KEYWORDS Raphanus sativus (radish)  
ORGANISM Raphanus sativus  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids II; Brassicales; Brassicaceae; Raphanus.  
REFERENCE 1 (bases 1 to 414)  
AUTHORS Broekaert,W.F., Cammue,B.P.A., Terras,F.R.G., Vanderleyden,J.,  
Osborn,R.W. and Rees,S.B.  
TITLE BIOCIDAL PROTEINS  
JOURNAL Patent: WO 9305153-A 33 18-MAR-1993;  
ICI PLC (GB)  
FEATURES  
source Location/Qualifiers  
1..414  
/organism="Raphanus sativus"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:3726"  
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Score: 442.00 Matches: 80  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
Gaps: 0  
US-09-759-584-49 (1-80) x A26875 (1-414)  
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Qy 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40  
Db 76 TTCGAAGCACCAACATATGTTGGAAGCAGAGATTTGTGGAAGGCCAAGTGGGACATGG 135  
Qy 41 SerGlyValCysGlyAsnAenAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60  
Db 136 TCAGGAGTCTGTGGAACCAATAACGATCGCAAGATCAAGTCAATTAACCTTGGAAGCA 195  
Qy 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80  
Db 196 CGACATGGATCTTGGCAACTATGCTTCCAGCTCACAAGTGTATCTGCTACTTTCCTTGT 255  
RESULT 5  
A39549  
LOCUS A39549 414 bp DNA linear PAT 05-MAR-1997  
DEFINITION Sequence 37 from Patent WO9416076.  
ACCESSION A39549  
VERSION A39549.1 GI:2295842  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 414)

AUTHORS Dubock,A.C., Powell,K.A. and Rees,S.B.  
TITLE ANTIMICROBIAL-PROTEIN-PRODUCING ENDOSYMBIOTIC MICROORGANISMS  
JOURNAL Patent: WO 9416076-A 37 21-JUL-1994;  
ZENECA LTD (GB)  
COMMENT Other publication AU 5820494 940815.  
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source Location/Qualifiers  
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/organism="unidentified"  
/mol\_type="unassigned DNA"  
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Score: 442.00 Matches: 80  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
Gaps: 0  
US-09-759-584-49 (1-80) x A39549 (1-414)  
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Db 16 ATGGCTAAGTTTGGCTCCATCGCAGCTCTTTTGTGCTCTTTTGTCTTCTTTTGTCTGT 75  
Qy 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40  
Db 76 TTCGAAGCACCAACATATGTTGGAAGCAGAGATTTGTGGAAGGCCAAGTGGGACATGG 135  
Qy 41 SerGlyValCysGlyAsnAenAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60  
Db 136 TCAGGAGTCTGTGGAACCAATAACGATCGCAAGATCAAGTCAATTAACCTTGGAAGCA 195  
Qy 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80  
Db 196 CGACATGGATCTTGGCAACTATGCTTCCAGCTCACAAGTGTATCTGCTACTTTCCTTGT 255  
RESULT 6  
A63404  
LOCUS A63404 414 bp DNA linear PAT 12-MAR-1998  
DEFINITION Sequence 19 from Patent WO9721814.  
ACCESSION A63404  
VERSION A63404.1 GI:3717176  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 unclassified sequences.  
AUTHORS Broekaert,W.F., De,S.G., Rees and Sarah,B.  
TITLE ANTIFUNGAL PROTEINS  
JOURNAL Patent: WO 9721814-A 19 19-JUN-1997;  
ZENECA LTD (GB)  
COMMENT Other publication AU 1105397 19970703.  
FEATURES  
source Location/Qualifiers  
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/mol\_type="unassigned DNA"  
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Score: 442.00 Matches: 80  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
Gaps: 0  
US-09-759-584-49 (1-80) x A63404 (1-414)  
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Qy      21  PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTtp 40
Db      76  TTCGAAGCACCACCAATGTTGGTGAAGCACAAGAAGTTGTGCGAAGGCCAAGTGGGACATGG 135
Qy      41  SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
Db      136  TCAGGAGTCTGTGGAAACATTAACGATCGAGATCAGTGCATTAACCTTGGAAGCA 195
Qy      61  ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
Db      196  CGACATGGATCTTGCAACTATGCTTCCAGCTCACAAGTGTATCTGCTACTTCTTCTTGT 255

RESULT 7
AR050153 LOCUS I23728 414 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 48 from patent US 5824869.
ACCESSION AR050153
VERSION AR050153.1 GI:5972145
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 414)
AUTHORS Broekaert,W.F., Cammue,B.P.A., Osborn,R.W., Rees,S.B.,
Terras,F.R.G. and Vanderleyden,J.
TITLE Biocidal proteins
JOURNAL Patent: US 5824869-A 48 20-OCT-1998;
FEATURES Location/Qualifiers
source 1. .414
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.: 1.08e-44 Length: 414
Score: 442.00 Matches: 80
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
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US-09-759-584-49 (1-80) x AR050153 (1-414)

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Qy      21  PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTtp 40
Db      76  TTCGAAGCACCACCAATGTTGGTGAAGCACAAGAAGTTGTGCGAAGGCCAAGTGGGACATGG 135
Qy      41  SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
Db      136  TCAGGAGTCTGTGGAAACATTAACGATCGAGATCAGTGCATTAACCTTGGAAGCA 195
Qy      61  ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
Db      196  CGACATGGATCTTGCAACTATGCTTCCAGCTCACAAGTGTATCTGCTACTTCTTCTTGT 255

RESULT 8
AR130272 LOCUS I23728 414 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 48 from patent US 6187904.
ACCESSION AR130272
VERSION AR130272.1 GI:14118169
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 414)
AUTHORS Broekaert,W.F., Cammue,B.P.A., Osborn,R.W., Rees,S.B.,
Terras,F.R.G. and Vanderleyden,J.
TITLE Biocidal proteins
JOURNAL Patent: US 5538525-A 48 23-JUL-1996;
FEATURES Location/Qualifiers
source 1. .414
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.: 1.08e-44 Length: 414
Score: 442.00 Matches: 80
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 6
Gaps: 0

US-09-759-584-49 (1-80) x I23728 (1-414)

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Qy      21  PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTtp 40
Db      76  TTCGAAGCACCACCAATGTTGGTGAAGCACAAGAAGTTGTGCGAAGGCCAAGTGGGACATGG 135
Qy      41  SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
Db      136  TCAGGAGTCTGTGGAAACATTAACGATCGAGATCAGTGCATTAACCTTGGAAGCA 195
Qy      61  ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
Db      196  CGACATGGATCTTGCAACTATGCTTCCAGCTCACAAGTGTATCTGCTACTTCTTCTTGT 255

RESULT 9
I23728 LOCUS I23728 414 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 48 from patent US 5538525.
ACCESSION I23728
VERSION I23728.1 GI:1603598
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 414)
AUTHORS Broekaert,W.F., Cammue,B.P.A., Osborn,R.W., Rees,S.B.,
Terras,F.R.G. and Vanderleyden,J.
TITLE Biocidal proteins
JOURNAL Patent: US 5538525-A 48 23-JUL-1996;
FEATURES Location/Qualifiers
source 1. .414
/organism="unknown"
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ORIGIN

Alignment Scores:
Pred. No.: 1.08e-44 Length: 414
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Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 6
Gaps: 0

US-09-759-584-49 (1-80) x I23728 (1-414)

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Qy      21  PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTtp 40
Db      76  TTCGAAGCACCACCAATGTTGGTGAAGCACAAGAAGTTGTGCGAAGGCCAAGTGGGACATGG 135
Qy      41  SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
Db      136  TCAGGAGTCTGTGGAAACATTAACGATCGAGATCAGTGCATTAACCTTGGAAGCA 195
Qy      61  ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
Db      196  CGACATGGATCTTGCAACTATGCTTCCAGCTCACAAGTGTATCTGCTACTTCTTCTTGT 255
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Terras,F.R.G. and Vanderleyden,J.
Biocidal proteins
Patent: US 6187904-A 48 13-FEB-2001;
Location/Qualifiers
1. .414
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.: 1.08e-44 Length: 414
Score: 442.00 Matches: 80
Percent Similarity: 100.0% Conservative: 0
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Query Match: 100.0% Indels: 0
DB: 6
Gaps: 0

US-09-759-584-49 (1-80) x AR130272 (1-414)

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Qy      21  PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTtp 40
Db      76  TTCGAAGCACCACCAATGTTGGTGAAGCACAAGAAGTTGTGCGAAGGCCAAGTGGGACATGG 135
Qy      41  SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
Db      136  TCAGGAGTCTGTGGAAACATTAACGATCGAGATCAGTGCATTAACCTTGGAAGCA 195
Qy      61  ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
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RESULT 9
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DEFINITION Sequence 48 from patent US 5538525.
ACCESSION I23728
VERSION I23728.1 GI:1603598
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 414)
AUTHORS Broekaert,W.F., Cammue,B.P.A., Osborn,R.W., Rees,S.B.,
Terras,F.R.G. and Vanderleyden,J.
TITLE Biocidal proteins
JOURNAL Patent: US 5538525-A 48 23-JUL-1996;
FEATURES Location/Qualifiers
source 1. .414
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.: 1.08e-44 Length: 414
Score: 442.00 Matches: 80
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 6
Gaps: 0

US-09-759-584-49 (1-80) x I23728 (1-414)

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Qy      21  PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTtp 40
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Db 136 TCAGGAGTCTGTGGAAACAATAACGATCAAGAAATCACTGATTAACCTTCAGAAAGCA 195

QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80

Db 196 CGACATGGATCTTGGCAACTATGTCTTCCAGCTCAAGTGTATCTGCTACTTTCCTTGT 255

RESULT 13

AR014693

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

ORIGIN

Alignment Scores:

Pred. No.: 285

Score: 433.00

Percent Similarity: 98.8%

Best Local Similarity: 97.5%

Query Match: 98.0%

Indels: 0

Gaps: 0

US-09-759-584-49 (1-80) x AR014693 (1-285)

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Db 31 ATGGCTTAAGTTTGGCTCCATCATCGCACTCTCTTTGGCTCTCTCTTCTTCTTGTCT 90

QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTTP 40

Db 91 TTCAGGAGTCTGCGAAACAACGATGCAAGAGTTGTGCCAAGGCCATCAGGAGCTTGG 150

QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60

Db 151 TCAGGAGTCTGCGAAACAACGATGCAAGAGTTGTGCCAAGGCCATCAGGAGCTTGG 210

QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80

Db 211 CGGCATGGATCTTGGCAACTACGTCTTCCAGCTCAAGTGCATCTGCTTTCATGC 270

RESULT 14

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

ORIGIN

Alignment Scores:

Pred. No.: 285

Score: 433.00

Percent Similarity: 98.8%

Best Local Similarity: 97.5%

Query Match: 98.0%

Indels: 0

Gaps: 0

US-09-759-584-49 (1-80) x AR014693 (1-285)

QY 1 MetAlaLysPheAlaSerIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 20

Db 31 ATGGCTTAAGTTTGGCTCCATCATCGCACTCTCTTTGGCTCTCTCTTCTTCTTGTCT 90

QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTTP 40

Db 91 TTCAGGAGTCTGCGAAACAACGATGCAAGAGTTGTGCCAAGGCCATCAGGAGCTTGG 150

QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60

Db 151 TCAGGAGTCTGCGAAACAACGATGCAAGAGTTGTGCCAAGGCCATCAGGAGCTTGG 210

QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80

Db 211 CGGCATGGATCTTGGCAACTACGTCTTCCAGCTCAAGTGCATCTGCTTTCATGC 270

RESULT 15

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

ORIGIN

Alignment Scores:

Pred. No.: 288

Score: 433.00

Percent Similarity: 98.8%

Best Local Similarity: 97.5%

Query Match: 98.0%

Indels: 0

Gaps: 0

US-09-759-584-49 (1-80) x A39553 (1-288)

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QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTTP 40

Db 103 TTCGAGGAGTCTGCGAAACAACGATGCAAGAGTTGTGCCAAGGCCATCAGGAGCTTGG 162

QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60

Db 163 TCAGGAGTCTGCGAAACAACGATGCAAGAGTTGTGCCAAGGCCATCAGGAGCTTGG 222

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ORIGIN

Alignment Scores:

Pred. No.: 285

Score: 433.00

Percent Similarity: 98.8%

Best Local Similarity: 97.5%

Query Match: 98.0%

Indels: 0

Gaps: 0

US-09-759-584-49 (1-80) x AR432393 (1-285)

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Db 31 ATGGCTTAAGTTTGGCTCCATCATCGCACTCTCTTTGGCTCTCTCTTCTTCTTGTCT 90

QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTTP 40

Db 91 TTCGAGGAGTCTGCGAAACAACGATGCAAGAGTTGTGCCAAGGCCATCAGGAGCTTGG 150

QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60

Db 151 TCAGGAGTCTGCGAAACAACGATGCAAGAGTTGTGCCAAGGCCATCAGGAGCTTGG 210

QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80

Db 211 CGGCATGGATCTTGGCAACTACGTCTTCCAGCTCAAGTGCATCTGCTTTCATGC 270

RESULT 15

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

ORIGIN

Alignment Scores:

Pred. No.: 288

Score: 433.00

Percent Similarity: 98.8%

Best Local Similarity: 97.5%

Query Match: 98.0%

Indels: 0

Gaps: 0

US-09-759-584-49 (1-80) x A39553 (1-288)

QY 1 MetAlaLysPheAlaSerIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 20

Db 43 ATGGCTTAAGTTTGGCTCCATCATCGCACTCTCTTTGGCTCTCTCTTCTTCTTGTCT 102

QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTTP 40

Db 103 TTCGAGGAGTCTGCGAAACAACGATGCAAGAGTTGTGCCAAGGCCATCAGGAGCTTGG 162

QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60

Db 163 TCAGGAGTCTGCGAAACAACGATGCAAGAGTTGTGCCAAGGCCATCAGGAGCTTGG 222

QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80  
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GenCore version 5.1.1.8  
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Title: US-09-759-584-49

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Post-processing: Minimum Match 0%

Maximum Match 100%

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- 8: Geneseqn2003as.\*
- 9: Geneseqn2003bs.\*
- 10: Geneseqn2003cs.\*
- 11: Geneseqn2003ds.\*
- 12: Geneseqn2004as.\*
- 13: Geneseqn2004bs.\*
- 14: Geneseqn2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	442	100.0	414	2	AAQ38650
2	442	100.0	414	2	AAQ70128
3	442	100.0	414	2	AAT72333
4	442	100.0	414	2	AAT68696

5	433	98.0	261	2	AAQ38652
6	433	98.0	288	2	AAQ70130
7	432	97.7	394	10	ADCS1221
8	432	97.7	394	13	ADU71300
9	425	96.2	426	10	ADCS1223
10	425	96.2	426	13	ADU71302
11	423	95.7	449	3	AAAS3190
12	418	94.6	575	3	AAZ99339
13	407	92.1	636	6	ABQ82690
14	407	92.1	414	3	AAZ39123
15	403	91.2	243	6	ABZ14241
16	403	91.2	243	6	ADG87651
17	403	91.2	243	6	ADG87824
18	403	91.2	243	8	ABZ42136
19	403	91.2	400	2	AAV10633
20	403	91.2	400	7	ADZ75091
21	402	91.0	243	6	ABQ82691
22	402	91.0	416	3	AAZ39124
23	397	89.8	243	6	ADG87728
24	397	89.8	243	6	ADG87923
25	397	89.8	243	8	ADA68378
26	397	89.8	403	2	AAV10632
27	396.5	89.7	270	2	AAZ94582
28	396.5	89.7	286	2	AAZ94574
29	396.5	89.7	481	2	AAZ99289
30	395	89.4	308	2	AAZ94577
31	384	86.9	500	2	AAZ94581
32	359	81.2	1973	3	AAZ94581
33	358	81.0	1616	2	AAV10646
34	304	68.8	159	10	ADG32304
35	304	68.8	984	10	ADG32343
36	304	68.8	987	10	ADG32350
37	304	68.8	987	10	ADG32348
38	303	68.6	534	3	AAZ99327
39	301.5	68.2	522	3	AAZ99324
40	301	68.1	485	3	AAZ99333
41	301	68.1	1093	3	AAZ99334
42	300	67.9	534	3	AAZ51396
43	300	67.9	534	3	AAZ99325
44	300	67.9	606	3	AAZ99326
45	296	67.0	153	13	ADR39326

ALIGNMENTS

RESULT 1  
AAQ38650  
ID AAQ38650 standard; DNA; 414 BP.

AC AAQ38650;

DT 25-MAR-2003 (revised)

DT 07-JUL-1993 (first entry)

DE Rs-APP1 cDNA.

XX Raphanus sativus; Brassica; Arabidopsis; Cnicus; Lathyrus; Clitoria; fungicide; bacteriocide; antibiotic; antifungal; gram positive; plant disease resistance; low toxicity.

XX Raphanus sativus.

XX Key Location/Qualifiers

FT CDS 16..256

FT /\*tag= a

XX WO9305153-A1.

XX 18-MAR-1993.

XX 27-AUG-1992; 92WO-GB001570.

XX 29-AUG-1991; 91GB-00018523.

```

PR 13-FEB-1992; 92GB-00003038.
XX 25-JUN-1992; 92GB-00013526.
XX (ICIL ) IMPERIAL CHEM IND PLC.
XX Broekaert WF, Cammue BPA, Osborn RW, Rees SB, Terras FRG;
XX Vanderleyden J;
XX WPI; 1993-100978/12.
XX Biocidal proteins isolated from seeds of plants - e.g. brassica or
PT dahlia, useful for increasing plants' resistance to fungal and bacterial
PT diseases.
XX Example 21; Fig 35; 110pp; English.
XX This cDNA represents the sequence of Rs-APF1 from Raphanus sativus. PCR
CC primer AAQ38640 was used together with AAQ38641 to generate a probe for
CC screening a Raphanus sativus seed cDNA library. This primer corresponds
CC to amino acids 2 to 7 of Rs-APF1 and has a sense orientation. The 144bp
CC product was partially re-amplified using AAQ38642 and AAQ38641 to give a
CC 123bp product, which was further reamplified with the same primers and
CC digoxigenin-11-dUTP instead of dTTP to give a digoxigenin labeled PCR
CC product. This was used to screen a lambda ZAPII cDNA library by in situ
CC plaque hybridisation. Positive plaques were purified and subjected to two
CC additional screening rounds with the same probe. Inserts were excised in
CC vivo into the pBluescript phagemid form with the aid of helper phage
CC R408. Inserts from 22 positive clones were excised by EcoRI digestion and
CC their size compared by agarose gel electrophoresis. Four clones had
CC insert sizes of approx. 400bp the others between 250-300bp. The inserts
CC of the 4 largest clones were then sequenced and found to differ only in
CC the length of their 5' and 3' UTR's. The longest sequence is given here.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4,04e-46 Length: 414
Score: 442.00 Matches: 80
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

US-09-759-584-49 (1-80) x AAQ38650 (1-414)
QY 1 MetAlaLysPheAlaSerIleIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 20
DB 16 ATGGCTAAAGTTTGGCTCCATCATCGCACTTCTTTTGTGCTCTTCTTTTGTGCTGCT 75
QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40
DB 76 TTCGAGACCAACAATATGTTGGAGACACAGAAAGTTTGGCAAGGCCAAGTGGGCATGG 135
QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
DB 136 TCAGGAGTCTGTGGAAACAATATACGATGCAAGATCAGTGCATTAACTTGAAGAAGCA 195
QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
DB 196 CGACATGGATCTTGGCAACTATGCTTCCAGCTCACAAAGTGTATCTGCTACTTCTCTGT 255

RESULT 2
AAQ70128
ID AAQ70128 standard; cDNA; 414 BP.
XX
XX AAQ70128;
XX 25-MAR-2003 (revised)
DT 14-FEB-1995 (first entry)
XX Antimicrobial Rs-APF1.
XX

KW Antimicrobial; Rs-APF1; symbiosis; disease-resistance; fungus-resistance;
XX Clavibacter xyl. subsp. cynodontis; Cxc; crop improvement; endophyte; ss.
XX Raphanus sativus.
XX W09416076-Al.
XX 21-JUL-1994.
XX 05-JAN-1994; 94WO-GB0000012.
XX 08-JAN-1993; 93GB-00000281.
XX (ZENE ) ZENECA LTD.
XX Dubock AC, Powell KA, Rees SB;
XX WPI; 1994-249223/30.
XX P-PSDB; AAR57325.
XX Antimicrobial protein producing endo-symbiotic microorganisms - is
PT produced by combining nucleic acids encoding the protein with an
PT endophyte, useful for protecting plant hosts from esp. fungal disease.
XX Disclosure; Page 31; 39pp; English.
XX Plant-derived antimicrobial proteins are expressed in endosymbiotic
CC Clavibacter xyl. subsp. cynodontis (Cxc). Plants or seeds treated with
CC recombinant Cxc are protected against fungal disease. A suitable
CC antimicrobial protein is Rs-APF1 from R. sativus. The full-length cDNA
CC sequence of Rs-APF1 is given in AAQ70128. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX SQ Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4,04e-46 Length: 414
Score: 442.00 Matches: 80
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

US-09-759-584-49 (1-80) x AAQ70128 (1-414)
QY 1 MetAlaLysPheAlaSerIleIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 20
DB 16 ATGGCTAAAGTTTGGCTCCATCATCGCACTTCTTTTGTGCTCTTCTTTTGTGCTGCT 75
QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40
DB 76 TTCGAGACCAACAATATGTTGGAGACACAGAAAGTTTGGCAAGGCCAAGTGGGCATGG 135
QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
DB 136 TCAGGAGTCTGTGGAAACAATATACGATGCAAGATCAGTGCATTAACTTGAAGAAGCA 195
QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
DB 196 CGACATGGATCTTGGCAACTATGCTTCCAGCTCACAAAGTGTATCTGCTACTTCTCTGT 255

RESULT 3
AAT72333
ID AAT72333 standard; cDNA; 414 BP.
XX
XX AAT72333;
XX 25-MAR-2003 (revised)
DT 19-JAN-1998 (first entry)
XX Raphanus sativus antifungal protein I (Rs-APF1) cDNA.
XX Antifungal protein; candida; fungal resistance; food additive; radish;
KW

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crop protection; plant defensin; bacterial protection; preservative; ss.

Raphanus sativus.

Key Location/Qualifiers  
CDS 16..258 /\*tag= a  
FT /transl\_except= (pos:85..87, aa:Glu)  
FT sig\_peptide 16..102 /\*tag= b  
FT mat\_peptide 103..255 /\*tag= c  
FT /product= "antifungal\_protein\_1"  
XX

W09721815-A2.  
XX  
XX  
XX PD 19-JUN-1997. 96WO-GB003068.  
XX PF 12-DEC-1996; 96WO-GB003068.  
XX PR 13-DEC-1995; 95GB-00025455.  
XX PR 28-MAR-1996; 96GB-00006552.  
XX PA (ZENE ) ZENECA LTD.  
XX  
XX Meloen RH, Puijk WC, Schaaper WM, Sijtsma L, Van Amerongen A;  
PI Broekaert W, Samblanx GW, Fant F, Borremans FAM, Rees SB;  
PI Van Gelder WMJ;  
XX  
XX WPI; 1997-332786/30.  
DR P-PSDB; AAW19280.  
XX  
XX Antifungal peptide derived from radish antifungal protein 2 - and related  
PT DNA, useful for producing plants with increased fungal resistance and as  
PT therapeutic or preservative agent.  
XX  
XX Claim 8; Fig 2; 65pp; English.  
XX  
XX This cDNA sequence encodes an Rhanopus sativus (radish) antifungal  
CC protein (Rs-AFP1). Analogues of the homologous protein, Rs-AFP2  
CC (AAW19281), have also been produced (see AAW19282-92, AAW19294-98,  
CC AAW19301-04, AAW19330-34 and AAW31765-834). Plants containing DNA  
CC sequences encoding these proteins have improved resistance to fungi.  
CC Compositions containing the peptides can be used to control fungi or  
CC bacteria in pharmaceutical (e.g. treatment of Candida infections) or  
CC preservative purposes (as food additives). In agriculture, the peptide  
CC may be used to improve disease resistance or disease tolerance of crops,  
CC either pre or post harvest. When applied to plants they may also have to  
CC curative as well as protective actions. The peptides may also be used to  
CC protect plants by introducing them, or a microorganism capable of  
CC expressing the peptide into the soil. (Updated on 25-MAR-2003 to correct  
CC PI field.)  
XX  
XX Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 4,04e-46 Length: 414  
Score: 442.00 Matches: 80  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
DB: Gaps: 0

US-09-759-584-49 (1-80) x AAT72333 (1-414)

Qy 1 MetAlalyPheAAlaSerilelleAlaLeuLeuPheAlaLaLeuValLeuPheAlaAa 20  
Db 16 ATGGCTAAGTTTGGTCATCATGCACCTCTTTTTGTGCTCTTGTTCTTTTGTGCT 75  
Qy 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40  
Db 76 TTCGAAGCACCAACTGTGTGAAGCAGAGAAGTTGTCGAAGGCCAAGTGGGACATGG 135

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|||||
16 ATGGCTAAGTTGGTCCATCGCATCTTTTGGTCTGCTGCTGCTGCTGCT 75
|||||
21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40
|||||
76 TTCGAAGCACCACCAATGTTGGGAAGCACAGAAAGTTTGGGAAGGCGCAAGTGGGACATGG 135
|||||
41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
|||||
136 TCAGGAGTCTGTGGAAACAATACGCATGCAAGATCAGTGCATTAACCTTTGGAAGAACA 195
|||||
61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
|||||
196 CGACATGGATCTTGCAACTATGCTTCCAGCTCACAAAGTGTATCTGCTACTTTCCTTCT 255

RESULT 5
AAQ38652
ID AAQ38652 standard; DNA; 261 BP.
XX
AC AAQ38652;
XX
DT 25-MAR-2003 (revised)
DT 07-JUL-1993 (first entry)
XX
DE RS-AFP2 cDNA.
XX
KW Raphanus sativus; Brassica; Arabidopsis; Chnicus; Lathyrus; Clitoria;
KW fungicide; bactericide; antibiotic; antifungal; gram positive;
KW plant disease resistance; low toxicity.
XX
OS Raphanus sativus.
XX
FH Key Location/Qualifiers
FT CDS 16..256
FT /*tag= a
XX
XX WO9305153-A1.
XX
PD 18-MAR-1993.
XX
XX
XX 27-AUG-1992; 92WO-GB001570.
XX
XX 29-AUG-1991; 91GB-00018523.
XX
XX 13-FEB-1992; 92GB-0003038.
XX
XX 25-JUN-1992; 92GB-00013526.
XX
XX (ICIL ) IMPERIAL CHEM IND PLC.
XX
XX Broekaert WF, Cammue BPA, Osborn RW, Rees SB, Terras FRG;
XX Vanderleyden J;
XX
XX WPI; 1993-100978/12.
XX
XX Biocidal proteins isolated from seeds of plants - e.g. brassica or
XX dahlia, useful for increasing plants' resistance to fungal and bacterial
XX diseases.
XX
XX Example 21; Fig 35; 110pp; English.
XX
XX This cDNA represents the sequence of Rs-AFP2 from Raphanus sativus. PCR
XX primer AAQ38640 was used together with AAQ38641 to generate a probe for
XX screening a Raphanus sativus seed cDNA library. This primer corresponds
XX to amino acids 2 to 7 of Rs-AFP1 and has a sense orientation. The 144bp
XX product was partially re-amplified using AAQ38642 and AAQ38641 to give a
XX 123bp product, which was further reamplified with the same primers and
XX digoxigenin-11-dUTP instead of dTTP to give a digoxigenin labeled PCR
XX product. This was used to screen a lambda ZAPII cDNA library by in situ
XX plaque hybridisation. Positive plaques were purified and subjected to two
XX additional screening rounds with the same probe. Inserts were excised in
XX vivo into the phiscript phagemid form with the aid of helper phage
XX R408. Inserts from 22 positive clones were excised by EcoRI digestion and
XX their size compared by agarose gel electrophoresis. Four clones had
XX insert sizes of approx. 400bp the others between 250-300bp. The inserts

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CC of the 4 largest clones were then sequenced and found to differ only in
CC the length of their 5' and 3' UTR's. The longest sequence was identified
CC as Rs-AFP1 (AAQ38650). Rs-AFP2 was seen to differ by only 2 amino acids
CC from Rs-AFP1, so the Rs-AFP1 cDNA was transformed to the Rs-AFP2
CC nucleotide sequence by PCR assisted site directed mutagenesis. (Updated
CC on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 261 BP; 67 A; 55 C; 59 G; 80 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 2,93e-45 Length: 261
Score: 433.00 Matches: 78
Percent Similarity: 98.8% Conservatives: 1
Best Local Similarity: 97.5% Mismatches: 1
Query Match: 98.0% Indels: 0
DB: 2 Gaps: 0
XX
US-09-759-584-49 (1-80) x AAQ38652 (1-261)
XX
QY 1 MetAlaLysPheAlaSerIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 20
DB 16 ATGGCTAAGTTGGTCCATCGCATCTTTTGGTCTGCTGCTGCTGCTGCTGCT 75
QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40
DB 76 TTCGAAGCACCACCAATGTTGGGAAGCACAGAAAGTTTGGGAAGGCGCAAGTGGGACATGG 135
QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
DB 136 TCAGGAGTCTGTGGAAACAATACGCATGCAAGATCAGTGCATTAACCTTTGGAAGAACA 195
QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
DB 196 CGACATGGATCTTGCAACTATGCTTCCAGCTCACAAAGTGTATCTGCTACTTTCCTTCT 255

RESULT 6
AAQ70130
ID AAQ70130 standard; cDNA; 288 BP.
XX
AC AAQ70130;
XX
DT 25-MAR-2003 (revised)
DT 14-FEB-1995 (first entry)
XX
DE Antimicrobial Rs-AFP2.
XX
KW Antimicrobial; Rs-AFP2; symbiosis; disease-resistance; fungus-resistance;
KW Clavibacter xyli subsp. cynodontis; Cxc; crop improvement; endophyte;
KW PCR; polymerase chain reaction; mutagenesis; ss.
XX
OS Raphanus sativus.
XX
XX WO9416076-A1.
XX
XX 21-JUL-1994.
XX
XX 05-JAN-1994; 94WO-GB0000012.
XX
XX 08-JAN-1993; 93GB-00000281.
XX
XX (ZENE ) ZENECA LTD.
XX
XX Dubock AC, Powell KA, Rees SB;
XX
XX WPI; 1994-249223/30.
XX
XX P-PSDB; AAR57327.
XX
XX Antimicrobial protein producing endo-symbiotic microorganisms - is
XX produced by combining nucleic acids encoding the protein with an
XX endophyte, useful for protecting plant hosts from eep. fungal disease.
XX
XX Disclosure; Page 33; 39pp; English.
XX
XX

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CC Plant-derived antimicrobial proteins are expressed in endosymbiotic  
 CC Clavibacter xyli subsp. cynodotis (Cxc). Plants or seeds treated with  
 CC recombinant Cxc are protected against fungal disease. A suitable  
 CC antimicrobial protein is Rs-AFP1 from R. sativus. The full-length cDNA  
 CC sequence of PCR assisted site-directed mutagenesis of Rs-AFP2 is given in  
 CC AAQ70130 and the deduced amino acid sequence in AA857327. (Updated on 25-  
 CC MAR-2003 to correct FN field.)  
 XX

SQ Sequence 288 BP; 70 A; 66 C; 69 G; 83 T; 0 U; 0 Other;

Alignment Scores: 3,35e-45 Length: 288  
 Pred. No.: 432.00 Matches: 78  
 Score: 98.8% Conservativity: 1  
 Percent Similarity: 97.5% Mismatches: 1  
 Best Local Similarity: 97.5% Indels: 0  
 Query Match: 98.0% Gaps: 0  
 DB: 2

US-09-759-584-49 (1-80) x AAQ70130 (1-288)

QY 1 MetAlaLysPheAlaSerIleAlaLeuPheAlaLeuValLeuPheAlaLa 20  
 DB 43 AUGGCTAAGTTTGCGTCCATCGCACTCTTTTGGTCTCTTCTTTTGGTCT 102  
 QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40  
 DB 103 TTCGAAGCACCACCAATGGTGGAGCACAGAACTTGTGCAAGGCGCAAGTGGGACATGG 162  
 QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60  
 DB 163 TCAGGAGTCTGTGGAACAATACGCATGCAAGATCAGTGCATTAGATTGGAAGAAGCA 222  
 QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80  
 DB 223 CGACATGGATCTTGCAACTATGCTTCCAGCTCACAGTGTATCTGCTACTTCTCTTGT 282

RESULT 7

ID ADC51221  
 AD51221 standard; DNA; 394 BP.

XX AC ADC51221;

XX 18-DEC-2003 (first entry)

XX Brassica oleracea defensin protein coding sequence.

XX antimicrobial protein; defensin; transgenic plant;  
 KW composite disease resistance; pathogenic bacteria;  
 KW rice white leaf blight; brown-stripe disease; glume blight;  
 KW seedling damping-off disease; filamentous fungi; rice blight;  
 KW sheath blight disease; leaf blight; gene; ds.

XX Brassica oleracea.

XX Key Location/Qualifiers  
 FH CDS 1..243  
 FT /\*tag= a  
 FT /product= "Brassica oleracea defensin protein"

XX JP2003088379-A.

XX 25-MAR-2003.

XX 18-SEP-2001; 2001JP-00283117.

XX 18-SEP-2001; 2001JP-00283117.

XX (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.

XX WPI; 2003-621123/59.

XX P-PSDB; ADC51222.

XX Novel protein from Brassica campestris, useful as antimicrobial against

PT plant pathogenic filamentous fungi or pathogenic bacteria, especially for  
 PT treating e.g. rice white leaf blight and sheath blight disease.

XX Claim 3; SEQ ID NO 1; 34pp; Japanese.

XX The invention comprises the amino acid and coding sequences of  
 CC antimicrobial (defensin) proteins from Brassica. The DNA and protein  
 CC sequences of the invention are useful for producing transgenic plants  
 CC with composite disease resistance, especially resistant to diseases  
 CC caused by pathogenic bacteria, such as: rice white leaf blight, brown-  
 CC stripe disease, glume blight, and seedling damping-off disease. As well  
 CC as diseases caused by filamentous fungi, such as: rice blight, sheath  
 CC blight disease, and leaf blight. The present DNA sequence encodes a  
 CC Brassica defensin protein of the invention.

SQ Sequence 394 BP; 116 A; 71 C; 82 G; 125 T; 0 U; 0 Other;

Alignment Scores: 6,86e-45 Length: 394  
 Pred. No.: 432.00 Matches: 78  
 Score: 97.5% Conservativity: 0  
 Percent Similarity: 97.5% Mismatches: 2  
 Best Local Similarity: 97.7% Indels: 0  
 Query Match: 10 Gaps: 0  
 DB: 0

US-09-759-584-49 (1-80) x ADC51221 (1-394)

QY 1 MetAlaLysPheAlaSerIleAlaLeuPheAlaLeuValLeuPheAlaLa 20  
 DB 1 ATGGCTAAGTTTGCTCCATCATCTGCTCTTTTGGTCTCTTGTCTTTTGGTCTGT 60  
 QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40  
 DB 61 CTCGAAGCACCACCAATGGTGGAGCACAGAACTTGTGCGAGGCGCAAGTGGGACATGG 120  
 QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60  
 DB 121 TCAGGAGTCTGTGGAACAATTAACGCATGCAAGATCAATTAACCTTGGAAGAAGCA 180  
 QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80  
 DB 181 CGACATGGATCTTGCAACTATGCTTCCAGCTCACAGTGTATTTGCTACTTCTCTTGT 240

RESULT 8

ADU71300

ID ADU71300 standard; cDNA; 394 BP.

XX AC ADU71300;

XX 10-FEB-2005 (first entry)

XX Brassica oleracea defensin protein coding sequence - SEQ ID 1.

XX antimicrobial; plant disease resistance; gene; ss; defensin.

XX Brassica oleracea.

XX Key Location/Qualifiers  
 FH CDS 1..243  
 FT /\*tag= a  
 FT /product= "Brassica oleracea defensin protein - SEQ ID 2"

XX JP2004329215-A.

XX 25-NOV-2004.

XX 07-JUN-2004; 2004JP-00168986.

XX 18-SEP-2001; 2001JP-00283117.

XX (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.

XX WPI; 2004-809169/80.

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DR P-PSDB; ADU71301.
XX
PT Novel Brassica sp. derived protein having antimicrobial activity, useful
PT for producing multiple disease resistant plants.
XX
PS Example 2; SEQ ID NO 1; 16pp; Japanese.
XX
XX The invention comprises the amino acid and coding sequence of an
CC antimicrobial protein obtained from Brassica sp. The DNA and protein
CC sequences of the invention are useful in the production of a multiple
CC disease resistant plant. The present cDNA sequence encodes the Brassica
CC oleracea defensin protein.
XX
SQ Sequence 394 BP; 116 A; 71 C; 82 G; 125 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6.86e-45 Length: 394
Score: 432.00 Matches: 78
Percent Similarity: 97.5% Conservativeness: 0
Best Local Similarity: 97.5% Mismatches: 2
Query Match: 97.7% Indels: 0
DB: 13 Gaps: 0

US-09-759-584-49 (1-80) x ADU71300 (1-394)
QY 1 MetAlaLysPheAlaSerIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 20
Db 1 ATGGCTAAGTTTGTGTCATCATGTCCTCTTTTGTCTCTTCTTCTTCTTCTTCTTCT 60
QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40
Db 61 CTCGAAGCACCACCAATGGTGGAGCACAGAGTGTGGAGAGGCCAAGTGGGACATGG 120
QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
Db 121 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA 180
QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
Db 181 CGACATGGATCTTGCACACTATGCTTCCAGCTCACAAGTGTATTTGCTACTTCCCTTGT 240

RESULT 9
ADU71302
ID ADC51223 standard; DNA; 426 BP.
AC ADC51223;
XX
XX 18-DEC-2003 (first entry)
DE Brassica defensin protein coding sequence.
XX
XX antimicrobial protein; defensin; transgenic plant;
XX composite disease resistance; pathogenic bacteria;
XX rice white leaf blight; brown-stripe disease; glume blight;
XX seedling damping-off disease; filamentous fungi; rice blight;
XX sheath blight disease; leaf blight; gene; ds.
XX
OS Brassica sp.
XX
XX Key Location/Qualifiers
XX CDS 1..243
XX /*tag= a
XX /product= "Brassica defensin protein"
XX
XX JP2003088379-A.
XX
XX 25-MAR-2003.
XX
XX 18-SEP-2001; 2001JP-00283117.
XX
XX 18-SEP-2001; 2001JP-00283117.
XX
XX (DOKU-) DOKURITSU GYOSSEI HOJIN NOGYO SEIBUTSU SH.

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XX WPI; 2003-621123/59.
DR P-PSDB; ADC51224.
XX
PT Novel protein from Brassica campestris, useful as antimicrobial against
PT plant pathogenic filamentous fungi or pathogenic bacteria, especially for
PT treating e.g. rice white leaf blight and sheath blight disease.
XX
PS Claim 3; SEQ ID NO 3; 34pp; Japanese.
XX
XX The invention comprises the amino acid and coding sequences of
CC antimicrobial (defensin) proteins from Brassica. The DNA and protein
CC sequences of the invention are useful for producing transformed plants
CC with composite disease resistance, especially resistant to diseases
CC caused by pathogenic bacteria, such as: rice white leaf blight, brown-
CC stripe disease, glume blight, and seedling damping-off disease. As well
CC as diseases caused by filamentous fungi, such as: rice blight, sheath
CC blight disease, and leaf blight. The present DNA sequence encodes a
CC Brassica defensin protein of the invention.
XX
SQ Sequence 426 BP; 142 A; 72 C; 84 G; 128 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 5.8e-44 Length: 426
Score: 425.00 Matches: 77
Percent Similarity: 96.2% Conservativeness: 0
Best Local Similarity: 96.2% Mismatches: 3
Query Match: 96.2% Indels: 0
DB: 10 Gaps: 0

US-09-759-584-49 (1-80) x ADC51223 (1-426)
QY 1 MetAlaLysPheAlaSerIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 20
Db 1 ATGGCCCAAGTTTGTGTCATCATGTCCTCTTTTGTCTCTTCTTCTTCTTCTTCTTCT 60
QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40
Db 61 TTCGAGGCCACCAACATGGTGGAGCACAGAGTGTGGAGAGGCCAAGTGGGACATGG 120
QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
Db 121 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA 180
QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
Db 181 CGACATGGATCTTGCACACTATGCTTCCAGCTCACAAGTGTATTTGCTACTTCCCTTGT 240

RESULT 10
ADU71302
ID ADU71302 standard; DNA; 426 BP.
XX
XX AC ADU71302;
XX
XX 10-FEB-2005 (first entry)
DE Brassica antimicrobial protein coding sequence - SEQ ID 3.
XX
XX antimicrobial; plant disease resistance; gene; ds.
XX
XX Brassica sp.
XX
XX Key Location/Qualifiers
XX CDS 1..243
XX /*tag= a
XX /product= "Brassica antimicrobial protein - SEQ ID 4"
XX
XX JP2004329215-A.
XX
XX 25-NOV-2004.
XX
XX 07-JUN-2004; 2004JP-00168986.
XX

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PR 18-SEP-2001; 2001JP-00283117.
XX
XX (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.
XX
XX WPI; 2004-809169/80.
XX
XX P-PSDB; ADU71303.
XX
XX Novel Brassica sp. derived protein having antimicrobial activity, useful
XX for producing multiple disease resistant plants.
XX
XX Claim 3; SEQ ID NO 3; 16pp; Japanese.
XX
XX The invention comprises the amino acid and coding sequence of an
XX antimicrobial protein obtained from Brassica sp. The DNA and protein
XX sequences of the invention are useful in the production of a multiple
XX disease resistant plant. The present DNA sequence encodes the Brassica
XX antimicrobial protein of the invention.
XX
XX SQ Sequence 426 BP; 142 A; 72 C; 84 G; 128 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 5.8e-44 Length: 426
XX Score: 425.00 Matches: 77
XX Percent Similarity: 96.2% Conservative: 0
XX Best Local Similarity: 96.2% Mismatches: 3
XX Query Match: 96.2% Indels: 0
XX DB: 13 Gaps: 0
XX
XX US-09-759-584-49 (1-80) x ADU71302 (1-426)
XX
XX QY 1 MetAlaLysPheAlaSerIleIleAlaLeuPheAlaAlaLeuValLeuPheAlaAla 20
XX Db 1 ATGGCCAAAGTTTGTCATCATTCATGCCCACTTTTGGCTGCTTGTCTTTAGTGCT 60
XX
XX QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTTP 40
XX Db 61 TTCAGGCACCACCAATGTGTGGAAGCACAGAAAGTTGTGAGAGGCCAAGTGGACATGG 120
XX
XX QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
XX Db 121 TCAGGAGTCTGTGGAACAATAACGCATGCAGATCAGTGCATTAACCTTGAGAAAGCA 180
XX
XX QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
XX Db 181 CGACATGGATCTTGCAACTATGTCTCCAGCTCACAGTGTATTGTCTACTTCCCTTGT 240
XX
XX RESULT 11
XX AAA53190
XX ID AAA53190 standard; DNA; 449 BP.
XX AC
XX AA53190;
XX
XX DT 06-OCT-2000 (first entry)
XX
XX DE Raphanus sativus antibacterial protein radishin encoding DNA SEQ ID NO:1.
XX
XX KW Raphanus sativus; antibacterial; plant; resistance; paddy; radishin;
XX pathogenic microbe; radish; rice blast disease; ds.
XX
XX OS Raphanus sativus.
XX
XX PN JP2000116379-A.
XX
XX PD 25-APR-2000.
XX
XX PF 09-OCT-1998; 98JP-00288472.
XX
XX PR 09-OCT-1998; 98JP-00288472.
XX
XX PA (TOYA-) TOYAMA KEN.
XX
XX WPI; 2000-389821/34.
XX
XX P-PSDB; AAY91117.
XX
XX Isolated DNA from Raphanus sativus used to transform a microbe and a
XX plant to produce an antibacterial protein used to increase resistance of
XX rice paddy against pathogenic microbes.
XX
XX Claim 1; Page 4; 7pp; Japanese.
XX
XX The present sequence encodes an antibacterial protein, designated
XX radishin, isolated from Raphanus sativus (radish). A phage or plasmid
XX comprising radishin can be used for increasing resistance of paddy and
XX rice blast disease against pathogenic microbes
XX
XX SQ Sequence 449 BP; 126 A; 78 C; 94 G; 151 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 1.11e-43 Length: 449
XX Score: 423.00 Matches: 75
XX Percent Similarity: 97.5% Conservative: 3
XX Best Local Similarity: 93.8% Mismatches: 2
XX Query Match: 93.8% Indels: 0
XX DB: 3 Gaps: 0
XX
XX US-09-759-584-49 (1-80) x AAA53190 (1-449)
XX
XX QY 1 MetAlaLysPheAlaSerIleIleAlaLeuPheAlaAlaLeuValLeuPheAlaAla 20
XX Db 41 ATGGCTAAAGTTTGCTTCCATCATTCCTCTCTTCGCTGCTCTTGTCTGCTTTTCTGCT 100
XX
XX QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTTP 40
XX Db 101 TTCGAGGACCAACCAATGTGTGGAAGCACAGAAAGTTGTGAGAGGCCAAGTGGACATGG 160
XX
XX QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
XX Db 161 TCAGGAGTCTGTGGAACAATAACGCATGCAGATCAGTGCATTCGACTTGAGAAAGCA 220
XX
XX QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
XX Db 221 CGACATGGTCTTGCAACTATGTCTCCAGCTCACAGTGTATTGTCTTATTTCCCTTGT 280
XX
XX RESULT 12
XX AAZ99339
XX ID AAZ99339 standard; DNA; 575 BP.
XX AC
XX AAZ99339;
XX
XX DT 03-JUL-2000 (first entry)
XX
XX DE DNA encoding a fusion protein of DmAMP1 and RsAPP2.
XX
XX KW Antimicrobial protein; AMP1; transgenic plant; linker peptide;
XX protein expression; plant defensin; RsAPP2; antifungal protein; AFP2; ss.
XX
XX OS Synthetic.
XX
XX OS Dahlia merckii.
XX
XX OS Unidentified.
XX
XX FH Key Location/Qualifiers
XX CDS 3...566
XX FT /*tag= a
XX FT /product= "fusion protein of DmAMP1 and RsAPP2"
XX
XX PN WO200011175-A1.
XX
XX PD 02-MAR-2000.
XX
XX PF 17-AUG-1999; 99WO-GB002716.
XX
XX PR 18-AUG-1998; 98GB-00018001.
XX
XX PR 04-DEC-1998; 98GB-00026753.
XX
XX (ZENE) ZENECA LTD.
XX

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PI Broekaert WF, Francois IEJA, De Bolle MFC, Evans IJ, Ray JA;  
 XX WPI; 2000-246564/21.  
 DR P-PSDB; AA184072.  
 XX  
 PT Improving expression of polyproteins in plants involves coexpression of  
 PT two or more proteins in plants within a single transcription unit.  
 XX  
 XX Disclosure; Fig 34; 151pp; English.  
 PS  
 XX The present sequence encodes a protein of the invention, comprising the  
 CC mature proteins of the plant defenses, the Dahlia antimicrobial protein  
 CC (AMP) 1 and the antifungal protein 2 (RsAFP2), linked by a linker  
 CC propeptide of the invention. The specification describes methods for  
 CC improving expression levels of one or more proteins in a transgenic  
 CC plant. The method comprises inserting a DNA sequence having a promoter  
 CC region operably linked to two or more protein encoding regions separated  
 CC by a DNA sequence coding for a linker propeptide and a terminator region.  
 CC The method is used to produce proteins in plants. The linker propeptide  
 CC comprising a cleavage site, whereby the expressed polypeptide is post-  
 CC translationally processed into the component protein molecules. The  
 CC propeptide sequence is rich in amino acids A, V, S and T and contains  
 CC dipeptidic sequences consisting of either two acidic, two basic or one  
 CC acidic and one basic residue as a cleavable linker sequence  
 XX  
 SQ Sequence 575 BP; 133 A; 137 C; 149 G; 156 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 6.64e-43 Length: 575  
 Score: 418.00 Matches: 76  
 Percent Similarity: 96.2% Conservative: 1  
 Best Local Similarity: 95.0% Mismatches: 3  
 Query Match: 94.6% Indels: 0  
 DB: 3 Gaps: 0

US-09-759-584-49 (1-80) x AAZ39339 (1-575)

QY 1 MetAlaLysPheAlaSerIleIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 20  
 Db 324 ATGGCTAAGTTTGGTCCATCATCGCACATCTTTTGGCTCTTTCTTTTGGCTGCT 383  
 QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40  
 Db 384 TTCGAGCACCACCAATCGTGGAGGCACAGAGCTTGTGCAAGGCCAAGTCGTACATG 443  
 QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60  
 Db 444 TCAGGAGTCTGTGGAAACAATACGCATCGCATGCAAGATCAGTGCAATTAGACTTGAAGAAGCA 503  
 QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80  
 Db 504 CGACATGGATCTTGCACATATCGTTTCCAGCTCAACAAGTGTATCTGCTACTTCTTGT 563

RESULT 13  
 ABQ82690  
 ID ABQ82690 standard; cDNA; 243 BP.  
 XX  
 AC ABQ82690;  
 XX  
 DT 02-JAN-2003 (first entry)  
 XX  
 DE Wasabia japonica gamma-thionin encoding cDNA SEQ ID NO:1.  
 XX  
 KW Wasabia japonica; gamma-thionin; plant; disease-resistant plant; gene;  
 KW ss.  
 XX  
 XX Eutrema wasabi.  
 XX  
 XX Key Location/Qualifiers  
 FH 1..243  
 FT CDS  
 FT /\*tag= a  
 FT /product= "gamma-thionin"  
 FT  
 XX

PN JP2002272292-A.  
 XX  
 PD 24-SEP-2002.  
 XX  
 PF 22-MAR-2001; 2001JP-00083526.  
 XX  
 PR 22-MAR-2001; 2001JP-00083526.  
 XX  
 XX (IWAT-) IWATE KEN.  
 XX  
 XX WPI; 2002-718704/78.  
 DR P-PSDB; ABP53725.  
 DR  
 PT A disease-resistant plant in which wasabi gamma-thionin gene is  
 PT introduced, creation of the disease-resistant plant.  
 XX  
 XX Claim 3; Page 8; 11pp; Japanese.  
 PS  
 XX The present invention describes a disease-resistant plant in which a  
 CC wasabi gamma-thionin gene is introduced. Also described is a method for  
 CC the creation of the above disease-resistant plant by introducing a wasabi  
 CC gamma-thionin gene to a plant. The present sequence encodes a Eutrema  
 CC wasabi (Wasabia japonica) gamma-thionin protein from the present  
 CC invention  
 XX  
 SQ Sequence 243 BP; 60 A; 54 C; 55 G; 74 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 4.99e-42 Length: 243  
 Score: 407.00 Matches: 72  
 Percent Similarity: 96.2% Conservative: 5  
 Best Local Similarity: 90.0% Mismatches: 3  
 Query Match: 92.1% Indels: 0  
 DB: 6 Gaps: 0

US-09-759-584-49 (1-80) x ABQ82690 (1-243)

QY 1 MetAlaLysPheAlaSerIleIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 20  
 Db 1 ATGGCTAAGTTTGGTCTTCTATCATCGCTCTTCTTCTGCTGCTCTTCTTCTTCTGCT 60  
 QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40  
 Db 61 TTTGAAGCACCACCAATCGTGGAGGCACAGAGTTGTGCAAGTCAAGTGGGACATGG 120  
 QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60  
 Db 121 TCAGGAGTCTGTGGAAACAATCGTGGCAAGATCAGTGCAATCAACCTTGAAGGAGCA 180  
 QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80  
 Db 181 CGACATGGATCTTGCACATATCTTCCATATCATCAGATGTATCTGTTACTTCCCATGT 240

RESULT 14  
 AAZ39123  
 ID AAZ39123 standard; cDNA to mRNA; 414 BP.  
 XX  
 AC AAZ39123;  
 XX  
 DT 15-SEP-2003 (revised)  
 DT 01-MAR-2000 (first entry)  
 XX  
 DE Wasabia japonica antibacterial protein encoding cDNA SEQ ID NO:1.  
 XX  
 KW Wasabia japonica; antibacterial; food additive; ds.  
 KW  
 XX Eutrema wasabi.  
 XX  
 XX Key Location/Qualifiers  
 FH 1..243  
 FT CDS  
 FT /\*tag= a  
 FT /product= "antibacterial protein"  
 FT  
 XX

PN JP11313678-A.  
XX 16-NOV-1999.  
XX 30-APR-1998; 98JP-00121303.  
XX 30-APR-1998; 98JP-00121303.  
XX (IWAT-) IWATE KEN.  
XX WPI; 2000-057353/05.  
XX P-PSDB; AA57564.  
XX An antibacterial protein gene of Wasabia japonica - useful as a food- or feed-additive.  
XX Claim 3; Page 12-13; 16pp; Japanese.  
XX The present sequence encodes an antibacterial protein isolated from Wasabia japonica. The antibacterial protein can be used as a food or feed additive. (Updated on 15-SEP-2003 to standardise OS field)  
XX Sequence 414 BP; 108 A; 79 C; 80 G; 147 T; 0 U; 0 Other;  
SQ  
Alignment Scores:  
Pred. No.: 1.03e-41 Length: 414  
Score: 407.00 Matches: 72  
Percent Similarity: 96.2% Conservative: 5  
Best Local Similarity: 90.0% Mismatches: 3  
Query Match: 92.1% Indels: 0  
DB: 3 Gaps: 0  
US-09-759-584-49 (1-80) x AA239123 (1-414)  
QY 1 MetAlaLysPheAlaSerIleAlaLeuPheAlaLeuValLeuPheAlaAla 20  
Db 1 ATGGCTAAGTTTGCCTTCTATCATCGCTCTCTTCGCTGCTCTTGTCTCTTTCTGCT 60  
QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40  
Db 61 TTGGAAGCACCATCAATGGTGGAGCGCAGAGTTGTGCGAGAGTCAAGTGGGACATGG 120  
QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60  
Db 121 TCAGGAGTCTGTGGAAACAACAATGCGTGCAGAGATCAGTGCATCAACCTTGAGGGAGCA 180  
QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80  
Db 181 CGACATGGATCTTGCACATATATCTTCCCATATACAGAGATGATCTGTACTTCCCATGT 240  
RESULT 15  
ABZ14241  
ID ABZ14241 standard; DNA; 243 BP.  
XX  
AC ABZ14241;  
XX  
XX 21-JAN-2003 (first entry)  
XX  
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 2046.  
XX  
KW Arabidopsis thaliana; plant; gene; stress; transgenic; ds.  
XX  
OS Arabidopsis thaliana.  
XX  
XX WO200216555-A2.  
XX  
XX 28-FEB-2002.  
XX  
XX 24-AUG-2001; 2001WO-US026685.  
XX  
XX 24-AUG-2000; 2000US-0227866P.  
XX 26-JAN-2001; 2001US-0264647P.  
XX 22-JUN-2001; 2001US-0300111P.

XX (SCRI ) SCRIPPS RES INST.  
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
XX  
PI Harper JF, Kreps J, Wang X, Zhu T;  
XX  
DR WPI; 2002-304127/34.  
XX  
XX Identifying a stress condition to which a plant cell has been exposed and producing plants with increased tolerance to these abiotic stresses.  
XX Claim 144; SEQ ID NO 2046; 577pp + Sequence Listing; English.  
XX The invention relates to identifying a stress condition to which a plant cell has been exposed, comprising: (a) contacting nucleic acid representative of expressed polynucleotides in the plant cell with an array or probes representative of the plant cell genome; and (b) detecting a profile of expressed polynucleotides in the plant cell characteristic of a stress response. The method is useful in the production of transgenic plants, cells and seeds and in producing plants with increased tolerance to abiotic stress. The present sequence is that of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used in methods of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office  
XX  
SQ Sequence 243 BP; 62 A; 57 C; 58 G; 66 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: 1.59e-41 Length: 243  
Score: 403.00 Matches: 71  
Percent Similarity: 95.0% Conservative: 5  
Best Local Similarity: 88.8% Mismatches: 4  
Query Match: 91.2% Indels: 0  
DB: 6 Gaps: 0  
US-09-759-584-49 (1-80) x ABZ14241 (1-243)  
QY 1 MetAlaLysPheAlaSerIleAlaLeuPheAlaLeuValLeuPheAlaAla 20  
Db 1 ATGGCTAAGTTTGCCTTCTATCATCACCTTATCTTCGCTGCTCTTGTCTCTTTGCTGT 60  
QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40  
Db 61 TTTCGACGACCGGCAATGGTGGAGCACAGAGTTGTGCGAGAGCCAGTGGGACATGG 120  
QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60  
Db 121 TCAGGGGTTTGGGAAACAGTAATGATGCAAGATCAGTGCATTAACCTTGAGGAGCC 180  
QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80  
Db 181 AAACATGGATCATGCACATATGCTTCCAGCACACAAGTGTATCTGTACGTCCCATGT 240  
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Job time : 453 secs

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: May 10, 2006, 06:02:00 ; Search time 3003.5 Seconds  
(without alignments)  
1869.302 Million cell updates/sec

Title: US-09-759-584-49  
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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
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Total number of hits satisfying chosen parameters: 82156650

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DLEXT=7

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3: gb\_est3:\*  
4: gb\_hc3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_est7:\*  
9: gb\_gse1:\*  
10: gb\_gse2:\*  
11: gb\_gse3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	436	98.6	413	7	CN826227
2	436	98.6	418	6	CD832625
3	436	98.6	420	6	CD833944
4	436	98.6	421	6	CD826491
5	436	98.6	421	6	CD831111
6	436	98.6	421	6	CD833977
7	436	98.6	422	6	CD833983

8	436	98.6	426	6	CD827413
9	436	98.6	438	6	CD831294
10	436	98.6	438	6	CD831479
11	436	98.6	453	6	CD834008
12	436	98.6	453	7	CN726424
13	436	98.6	456	7	CN726661
14	436	98.6	480	6	CD828332
15	436	98.6	553	6	CD831014
16	435	98.4	409	6	CD833779
17	435	98.4	408	6	CD834090
18	435	98.4	446	6	CD834068
19	435	98.4	447	6	CD832592
20	435	98.4	450	6	CD834611
21	435	98.4	452	6	CD832071
22	435	98.4	458	6	CD834994
23	435	98.4	470	6	CD831680
24	435	98.4	484	7	CN726241
25	435	98.4	485	7	CN726374
26	435	98.4	547	7	CN726625
27	435	98.4	566	7	CN725823
28	435	98.4	592	7	CN726094
29	435	98.4	597	7	CN726329
30	433	98.0	419	6	CD834168
31	431	97.5	458	7	CN726701
32	430	97.3	425	6	CD834852
33	430	97.3	427	6	CD833613
34	430	97.3	444	8	DN778142
35	430	97.3	449	6	CD833047
36	430	97.3	481	7	CN726255
37	430	97.3	484	7	CN726272
38	430	97.3	523	6	CD833661
39	430	97.3	543	6	CD828840
40	427	96.6	421	6	CD837517
41	427	96.6	424	6	CD833048
42	426	96.4	522	6	CD833938
43	426	96.4	646	6	CD829429
c	44	95.9	376	7	CN827135
45	424	95.9	409	6	CD832294

ALIGNMENTS

RESULT 1

CN826227  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

CN826227  
EL1386 Brassica embryo library (EL) Brassica napus cDNA clone  
EL1386 complete, mRNA sequence.  
CN826227.1 GI:65296011  
EST.  
Brassica napus (rape)  
Brassica napus

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Sharpe,A.G., Gjetvaj,B., Durkin,J. and Lydiate,D.J.  
Brassica napus ESTs  
Unpublished (2004)  
Contact: Sharpe, A.G.  
Molecular Genetics  
Agriculture & Agri-Food Canada  
107 Science Place, Saskatoon, Saskatchewan, Canada, S7N0X2  
Tel: 306 956 7271  
Fax: 306 956 7247  
Email: sharpe@agr.gc.ca

Seq primer: M13 Forward and T7.  
Location/Qualifiers  
1. 413  
/organism="Brassica napus"  
/mol\_type="mRNA"  
/cultivar="DH12075 (double haploid line from Cresor x Westar cross)"

FEATURES  
source

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/db_xref="taxon:3708"
/clone="EL1386"
/dev_stage="Mid to late embryos (4-6 mg)"
/lab_host="E. coli Electromax DH5 alpha-e (Invitrogen)"
/clone_lib="Brassica embryo library (EL)"
/note="Organ: Embryos without seed coat; Vector: pSPORT1 (modified: GCGCGGCCCGACTAGTGAGTC*cgagcgtggTCGAC); Site_1: NotI; Site_2: SalI; Seeds were collected by Dr. Francois Ouellet when they were still very green (mid to large stage, cotyledons were formed). The seed coats were removed and the remaining tissue was used for cDNA library construction. mRNA was poly-A primed using SuperScript plasmid system cDNA Synthesis and Cloning kit (Invitrogen) After initial screening, the most abundant redundant clones were screened out using 22 oligos designed to match napins (including albumins), cruciferins, oleosins, trypsin inhibitor 2, cytosolic GAPDH, cyclophilins, HSP70, desaturase, and CAB (LHCP)."

```

## ORIGIN

Alignment Scores:  
 Pred. No.: 1.65e-41 Length: 413  
 Score: 436.00 Matches: 79  
 Percent Similarity: 98.8% Conservative: 0  
 Best Local Similarity: 98.8% Mismatches: 1  
 Query Match: 98.6% Indels: 0  
 DB: 7 Gaps: 0

US-09-759-584-49 (1-80) x CN826227 (1-413)

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QY 1 MetAlaLysPheAlaSerIleAlaLeuLeuPheAlaLeuValLeuPheAlaLa 20
DB 28 ATGGCTAAGTTGCTTCCATCATTCCTTCTTTTGTCTCTTCTTCTTCTTCT 87
QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40
DB 88 CTCGAAGCACCACCAATGTTGGAGCACAGAGTTGTGGAGAGCCCAAGTGGACATGG 147
QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
DB 148 TCAGGAGTCTGTGGAAACAATACGCATCGAAGATCATGTCATTAACCTTCGAGAAGCA 207
QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
DB 208 CGACATGGATCTTGCAACTATGCTTCCAGCTCACAGTGATTTGCTACTTCCCTTGT 267

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RESULT 2
CD832625 418 bp mRNA linear EST 10-JUL-2003
LOCUS
DEFINITION
BN40.064A14F011227 BN40 Brassica napus cDNA clone BN40064A14, mRNA
sequence.
ACCESSION
CD832625
VERSION
CD832625.1 GI:32514565
KEYWORDS
EST.
SOURCE
Brassica napus (rape)
ORGANISM
Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
1 (bases 1 to 418)
Genoplate.
Genoplate, a major partnership french program in plant genomics
Unpublished (2003)
Contact: Genoplate
Genoplate
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplate' (http://www.genoplate.com
and http://genoplate-info.infobiogen.fr).

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FEATURES
SOURCE
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/organism="Brassica napus"
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/clone="BN40064A14"
/tissue_type="seed"
/clone_lib="BN45"

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Alignment Scores:  
 Pred. No.: 1.68e-41 Length: 420

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## ORIGIN

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 Score: 436.00 Matches: 79  
 Percent Similarity: 98.8% Conservative: 0  
 Best Local Similarity: 98.8% Mismatches: 1  
 Query Match: 98.6% Indels: 0  
 DB: 6 Gaps: 0

US-09-759-584-49 (1-80) x CD832625 (1-418)

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QY 1 MetAlaLysPheAlaSerIleAlaLeuLeuPheAlaLaLeuValLeuPheAlaLa 20
DB 53 ATGGCAAGTTGCTTCCATCATTCCTTCTTTTGTCTCTTCTTCTTCTTCTTCT 112
QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40
DB 113 CTCGAAGCACCACCAATGTTGGAGCACAGAGTTGTGGAGAGCCCAAGTGGACATGG 172
QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
DB 173 TCAGGAGTCTGTGGAAACAATACGCATCGAAGATCATGTCATTAACCTTCGAGAAGCA 232
QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
DB 233 CGACATGGATCTTGCAACTATGCTTCCAGCTCACAGTGATTTGCTACTTCCCTTGT 292

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## RESULT 3

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CD833944 420 bp mRNA linear EST 10-JUL-2003
LOCUS
DEFINITION
BN45.040B07F011019 BN45 Brassica napus cDNA clone BN45040B07, mRNA
sequence.
ACCESSION
CD833944
VERSION
CD833944.1 GI:32515884
KEYWORDS
EST.
SOURCE
Brassica napus (rape)
ORGANISM
Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
1 (bases 1 to 420)
Genoplate.
Genoplate, a major partnership french program in plant genomics
Unpublished (2003)
Contact: Genoplate
Genoplate
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplate' (http://www.genoplate.com
and http://genoplate-info.infobiogen.fr).

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FEATURES
SOURCE
1. .420
/organism="Brassica napus"
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/cultivar="Jet Neuf"
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/clone="BN45040B07"
/tissue_type="seed"
/clone_lib="BN45"

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## FEATURES

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SOURCE
1. .420
/organism="Brassica napus"
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/cultivar="Jet Neuf"
/db_xref="taxon:3708"
/clone="BN45040B07"
/tissue_type="seed"
/clone_lib="BN45"

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Alignment Scores:  
 Pred. No.: 1.68e-41 Length: 420



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Score: 436.00 Matches: 79
Percent Similarity: 98.8% Conservative: 0
Best Local Similarity: 98.8% Mismatches: 1
Query Match: 98.6% Indels: 0
DB: 6 Gaps: 0

US-09-759-584-49 (1-80) x CD833944 (1-420)

QY 1 MetAlaLysPheAlaSerIleLeAlaLeuPheAlaLeuValLeuPheAlaAla 20
Db 50 ATGGCTAAGTTGCTTCCATCATTCGCTACTTTTGGCTGCTCTTGTCTCTTTCGCTGCT 109
QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40
Db 110 CTCGAAGCACCACCAATGTTGGAGCACAGAAAGTTGTGCGAGAGGCCAAGTGGGACATGG 169
QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
Db 170 TCAGGAGTCTGTGGAAACAATTAACGATGCAAGATCAGTGCATTAACCTTGAGAAAGCA 229
QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
Db 230 CGACATGGATCTTGCAACTATGCTTCCAGCTCACAAGTGATTTGCTACTTCCCTTGT 289

RESULT 4
CD826491 421 bp mRNA linear EST 10-JUL-2003
LOCUS BN25_064A05F020416 BN25 Brassica napus cDNA clone BN25064A05, mRNA
DEFINITION
ACCESSION CD826491
VERSION CD826491.1 GI:32508431
KEYWORDS EST.
SOURCE Brassica napus (rape)
ORGANISM Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicotyledons;
Rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 421)
AUTHORS Genoplante, a major partnership french program in plant genomics
TITLE Genoplante.
JOURNAL Unpublished (2003)
COMMENT Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).

FEATURES
source
1..421
/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jet Neuf"
/db_xref="taxon:3708"
/clone="BN25064A05"
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Alignment Scores:
Pred. No.: 1.69e-41 Length: 421
Score: 436.00 Matches: 79
Percent Similarity: 98.8% Conservative: 0
Best Local Similarity: 98.8% Mismatches: 1
Query Match: 98.6% Indels: 0
DB: 6 Gaps: 0

US-09-759-584-49 (1-80) x CD826491 (1-421)

QY 1 MetAlaLysPheAlaSerIleLeAlaLeuPheAlaLeuValLeuPheAlaAla 20
Db 51 ATGGCTAAGTTGCTTCCATCATTCGCTACTTTTGGCTGCTCTTGTCTCTTTCGCTGCT 110
QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40
Db 111 CTCGAAGCACCACCAATGTTGGAGCACAGAAAGTTGTGCGAGAGGCCAAGTGGGACATGG 170
QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
Db 171 TCAGGAGTCTGTGGAAACAATTAACGATGCAAGATCAGTGCATTAACCTTGAGAAAGCA 230
QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
Db 231 CGACATGGATCTTGCAACTATGCTTCCAGCTCACAAGTGATTTGCTACTTCCCTTGT 290

RESULT 5
CD831111 421 bp mRNA linear EST 10-JUL-2003
LOCUS BN40_058A09F011019 BN40 Brassica napus cDNA clone BN40058A09, mRNA
DEFINITION
ACCESSION CD831111
VERSION CD831111.1 GI:32513051
KEYWORDS EST.
SOURCE Brassica napus (rape)
ORGANISM Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 421)
AUTHORS Genoplante, a major partnership french program in plant genomics
TITLE Genoplante.
JOURNAL Unpublished (2003)
COMMENT Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).

FEATURES
source
1..421
/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jet Neuf"
/db_xref="taxon:3708"
/clone="BN40058A09"
/tissue_type="seed"
/clone_lib="BN40"

ORIGIN
Alignment Scores:
Pred. No.: 1.69e-41 Length: 421
Score: 436.00 Matches: 79
Percent Similarity: 98.8% Conservative: 0
Best Local Similarity: 98.8% Mismatches: 1
Query Match: 98.6% Indels: 0
DB: 6 Gaps: 0

US-09-759-584-49 (1-80) x CD831111 (1-421)

QY 1 MetAlaLysPheAlaSerIleLeAlaLeuPheAlaLeuValLeuPheAlaAla 20
Db 51 ATGGCTAAGTTGCTTCCATCATTCGCTACTTTTGGCTGCTCTTGTCTCTTTCGCTGCT 110
QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40
Db 111 CTCGAAGCACCACCAATGTTGGAGCACAGAAAGTTGTGCGAGAGGCCAAGTGGGACATGG 170
QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
Db 171 TCAGGAGTCTGTGGAAACAATTAACGATGCAAGATCAGTGCATTAACCTTGAGAAAGCA 230
QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
Db 231 CGACATGGATCTTGCAACTATGCTTCCAGCTCACAAGTGATTTGCTACTTCCCTTGT 290

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Db 231 CGACATGGATCTTGCAACTATGCTTCCAGCTCACAAGTGATTTGCTACTTCCCTTGT 290

RESULT 6
CD833977
LOCUS
DEFINITION
  CD833977 421 bp mRNA linear EST 10-JUL-2003
  BN45.040D05F011019 BN45 Brassica napus cDNA clone BN45040D05, mRNA
  sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
  CD833977.1 GI:32515917
  Brassica napus (rape)
ORGANISM
  Brassica napus
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
  rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
  1 (bases 1 to 421)
  Genoplatne, a major partnership french program in plant genomics
  Unpublished (2003)
  Contact: Genoplatne
  Location/Qualifiers
    source
      1..421
        /organism="Brassica napus"
        /mol_type="mRNA"
        /cultivar="Jet Neuf"
        /db_xref="taxon:3708"
        /clone="BN45040D05"
        /tissue_type="seed"
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ORIGIN
Alignment Scores:
Pred. No.: 1.69e-41 Length: 421
Score: 436.00 Matches: 79
Percent Similarity: 98.8% Conservative: 0
Best Local Similarity: 98.8% Mismatches: 1
Query Match: 98.6% Indels: 0
DB: 6 Gaps: 0

US-09-759-584-49 (1-80) x CD833977 (1-421)

QY 1 MetAlaLysPheAlaSerIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 20
|||||
Db 51 ATGGCTAAGTTTGCTTCCATCATGCTCTTTTGGCTGCTCTTCTTTCGCTGCT 110
|||||

QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40
|||||
Db 111 CTCGAAGCACCACCAATGTTGGGAAGCACAGAAAGTTGTGCGAGAGCCAAAGTGGACATGG 170
|||||

QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
|||||
Db 171 TCAGGAGTCTGTGGAAACAATAACCGATGCAAGAATCAGTGCATTAAACCTTGAGAAAGCA 230
|||||

QY 61 AtgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
|||||
Db 231 CGACATGGATCTTGCAACTATGCTTCCAGCTCACAAGTGATTTGCTACTTCCCTTGT 290

RESULT 7
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LOCUS
DEFINITION
  CD833983 422 bp mRNA linear EST 10-JUL-2003
  BN45.040D11F011019 BN45 Brassica napus cDNA clone BN45040D11, mRNA
  sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
  CD833983.1 GI:32515923
  Brassica napus (rape)
ORGANISM
  Brassica napus
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
  rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
  1 (bases 1 to 422)
  Genoplatne, a major partnership french program in plant genomics
  Unpublished (2003)
  Contact: Genoplatne
  Location/Qualifiers
    source
      1..422
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        /mol_type="mRNA"
        /cultivar="Jet Neuf"
        /db_xref="taxon:3708"
        /clone="BN45040D11"
        /tissue_type="seed"
        /clone_lib="BN45"
ORIGIN
Alignment Scores:
Pred. No.: 1.69e-41 Length: 422
Score: 436.00 Matches: 79
Percent Similarity: 98.8% Conservative: 0
Best Local Similarity: 98.8% Mismatches: 1
Query Match: 98.6% Indels: 0
DB: 6 Gaps: 0

US-09-759-584-49 (1-80) x CD833983 (1-422)

QY 1 MetAlaLysPheAlaSerIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 20
|||||
Db 51 ATGGCTAAGTTTGCTTCCATCATGCTCTTTTGGCTGCTCTTCTTTCGCTGCT 110
|||||

QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40
|||||
Db 111 CTCGAAGCACCACCAATGTTGGGAAGCACAGAAAGTTGTGCGAGAGCCAAAGTGGACATGG 170
|||||

QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
|||||
Db 171 TCAGGAGTCTGTGGAAACAATAACCGATGCAAGAATCAGTGCATTAAACCTTGAGAAAGCA 230
|||||

QY 61 AtgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
|||||
Db 231 CGACATGGATCTTGCAACTATGCTTCCAGCTCACAAGTGATTTGCTACTTCCCTTGT 290

RESULT 8
CD827413
LOCUS
DEFINITION
  CD827413 426 bp mRNA linear EST 10-JUL-2003
  BN25.067G02F020123 BN25 Brassica napus cDNA clone BN25067G02, mRNA
  sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
  CD827413.1 GI:32509353
  Brassica napus (rape)
ORGANISM
  Brassica napus
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
  rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
  1 (bases 1 to 426)
  Genoplatne, a major partnership french program in plant genomics
  Unpublished (2003)
  Contact: Genoplatne
  Location/Qualifiers
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        /db_xref="taxon:3708"
        /clone="BN45040D11"
        /tissue_type="seed"
        /clone_lib="BN45"
ORIGIN
Alignment Scores:
Pred. No.: 1.69e-41 Length: 426
Score: 436.00 Matches: 79
Percent Similarity: 98.8% Conservative: 0
Best Local Similarity: 98.8% Mismatches: 1
Query Match: 98.6% Indels: 0
DB: 6 Gaps: 0

US-09-759-584-49 (1-80) x CD833983 (1-422)

QY 1 MetAlaLysPheAlaSerIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 20
|||||
Db 51 ATGGCTAAGTTTGCTTCCATCATGCTCTTTTGGCTGCTCTTCTTTCGCTGCT 110
|||||

QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40
|||||
Db 111 CTCGAAGCACCACCAATGTTGGGAAGCACAGAAAGTTGTGCGAGAGCCAAAGTGGACATGG 170
|||||

QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
|||||
Db 171 TCAGGAGTCTGTGGAAACAATAACCGATGCAAGAATCAGTGCATTAAACCTTGAGAAAGCA 230
|||||

QY 61 AtgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
|||||
Db 231 CGACATGGATCTTGCAACTATGCTTCCAGCTCACAAGTGATTTGCTACTTCCCTTGT 290
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ORGANISM
  Brassica napus
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
  rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
  1 (bases 1 to 422)
  Genoplatne, a major partnership french program in plant genomics
  Unpublished (2003)
  Contact: Genoplatne
  Location/Qualifiers
    source
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        /organism="Brassica napus"
        /mol_type="mRNA"
        /cultivar="Jet Neuf"
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        /tissue_type="seed"
        /clone_lib="BN45"
ORIGIN
Alignment Scores:
Pred. No.: 1.69e-41 Length: 422
Score: 436.00 Matches: 79
Percent Similarity: 98.8% Conservative: 0
Best Local Similarity: 98.8% Mismatches: 1
Query Match: 98.6% Indels: 0
DB: 6 Gaps: 0

US-09-759-584-49 (1-80) x CD833983 (1-422)

QY 1 MetAlaLysPheAlaSerIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 20
|||||
Db 51 ATGGCTAAGTTTGCTTCCATCATGCTCTTTTGGCTGCTCTTCTTTCGCTGCT 110
|||||

QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40
|||||
Db 111 CTCGAAGCACCACCAATGTTGGGAAGCACAGAAAGTTGTGCGAGAGCCAAAGTGGACATGG 170
|||||

QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
|||||
Db 171 TCAGGAGTCTGTGGAAACAATAACCGATGCAAGAATCAGTGCATTAAACCTTGAGAAAGCA 230
|||||

QY 61 AtgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
|||||
Db 231 CGACATGGATCTTGCAACTATGCTTCCAGCTCACAAGTGATTTGCTACTTCCCTTGT 290

RESULT 8
CD827413
LOCUS
DEFINITION
  CD827413 426 bp mRNA linear EST 10-JUL-2003
  BN25.067G02F020123 BN25 Brassica napus cDNA clone BN25067G02, mRNA
  sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
  CD827413.1 GI:32509353
  Brassica napus (rape)
ORGANISM
  Brassica napus
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
  rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
  1 (bases 1 to 426)
  Genoplatne, a major partnership french program in plant genomics
  Unpublished (2003)
  Contact: Genoplatne
  Location/Qualifiers
    source
      1..426
        /organism="Brassica napus"
        /mol_type="mRNA"
        /cultivar="Jet Neuf"
        /db_xref="taxon:3708"
        /clone="BN45040D11"
        /tissue_type="seed"
        /clone_lib="BN45"
ORIGIN
Alignment Scores:
Pred. No.: 1.69e-41 Length: 426
Score: 436.00 Matches: 79
Percent Similarity: 98.8% Conservative: 0
Best Local Similarity: 98.8% Mismatches: 1
Query Match: 98.6% Indels: 0
DB: 6 Gaps: 0

US-09-759-584-49 (1-80) x CD833983 (1-422)

QY 1 MetAlaLysPheAlaSerIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 20
|||||
Db 51 ATGGCTAAGTTTGCTTCCATCATGCTCTTTTGGCTGCTCTTCTTTCGCTGCT 110
|||||

QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40
|||||
Db 111 CTCGAAGCACCACCAATGTTGGGAAGCACAGAAAGTTGTGCGAGAGCCAAAGTGGACATGG 170
|||||

QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
|||||
Db 171 TCAGGAGTCTGTGGAAACAATAACCGATGCAAGAATCAGTGCATTAAACCTTGAGAAAGCA 230
|||||

QY 61 AtgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
|||||
Db 231 CGACATGGATCTTGCAACTATGCTTCCAGCTCACAAGTGATTTGCTACTTCCCTTGT 290
```

Tel: 33 1 69 47 54 00  
 Fax: 33 1 69 47 54 10  
 This sequence has been generated in the framework of the french  
 plant genomics programme 'Genoplante' (<http://www.genoplante.com>)  
 and <http://genoplante-info.infobiogen.fr/>.

## FEATURES

source  
 Location/Qualifiers  
 1. .426  
 /organism="Brassica napus"  
 /mol\_type="mRNA"  
 /cultivar="Jet Neuf"  
 /db\_xref="taxon:3708"  
 /clone="BN25067G02"  
 /tissue\_type="seed"  
 /clone\_lib="BN25"

## ORIGIN

Alignment Scores:  
 Pred. No.: 1,71e-41 Length: 426  
 Score: 436.00 Matches: 79  
 Percent Similarity: 98.8% Conservative: 0  
 Best Local Similarity: 98.8% Mismatches: 1  
 Query Match: 98.6% Indels: 0  
 DB: 6 Gaps: 0

US-09-759-584-49 (1-80) x CD827413 (1-426)

QY 1 MetAlaLySePheAlaSerIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 20  
 |||||  
 Db 51 ATGGCTAAGTTGCTTCCATCATTTGCCCTACTTTTGTGCTCTTGTCTTTTGGCTGCT 110  
 |||||

QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40  
 |||||  
 Db 111 CTCGAAGCACCACCAACATGCTGGAGCACAGAAAGTTGTGCGAGAGCCAAAGTGGGACATGG 170  
 |||||

QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60  
 |||||  
 Db 171 TCAGGAGTCTGTGGAAACAAATACGCATGCAAGATCAAGTGCATTAACTTGGAAAGCA 230  
 |||||

QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80  
 |||||  
 Db 231 CGACATGGATCTTGCACTATGCTTCCAGCTCAAGTGTATTGTCTACTTCCCTTGT 290  
 |||||

RESULT 9  
 CD831294  
 LOCUS  
 DEFINITION  
 BN40.058N13F011019 BN40 Brassica napus cDNA clone BN40058N13, mRNA  
 sequence.  
 ACCESSION  
 CD831294  
 VERSION  
 CD831294.1 GI:32513234  
 KEYWORDS  
 EST.  
 SOURCE  
 Brassica napus (rape)  
 ORGANISM  
 Brassica napus  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
 1 (bases 1 to 438)  
 Genoplante.  
 Genoplante, a major partnership french program in plant genomics  
 Unpublished (2003)  
 Contact: Genoplante  
 Genoplante  
 93, rue Henri Rochefort 91025 EVRY CEDEX France  
 Tel: 33 1 69 47 54 00  
 Fax: 33 1 69 47 54 10  
 This sequence has been generated in the framework of the french  
 plant genomics programme 'Genoplante' (<http://www.genoplante.com>)  
 and <http://genoplante-info.infobiogen.fr/>.

## FEATURES

source  
 Location/Qualifiers  
 1. .438  
 /organism="Brassica napus"  
 /mol\_type="mRNA"  
 /cultivar="Jet Neuf"  
 /db\_xref="taxon:3708"

/clone="BN40058N13"  
 /tissue\_type="seed"  
 /clone\_lib="BN40"

## ORIGIN

Alignment Scores:  
 Pred. No.: 1,78e-41 Length: 438  
 Score: 436.00 Matches: 79  
 Percent Similarity: 98.8% Conservative: 0  
 Best Local Similarity: 98.8% Mismatches: 1  
 Query Match: 98.6% Indels: 0  
 DB: 6 Gaps: 0

US-09-759-584-49 (1-80) x CD831294 (1-438)

QY 1 MetAlaLySePheAlaSerIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 20  
 |||||  
 Db 51 ATGGCTAAGTTGCTTCCATCATTTGCCCTACTTTTGTGCTCTTGTCTTTTGGCTGCT 110  
 |||||

QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40  
 |||||  
 Db 111 CTCGAAGCACCACCAACATGCTGGAGCACAGAAAGTTGTGCGAAAGCCCAAGTGGGACATGG 170  
 |||||

QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60  
 |||||  
 Db 171 TCAGGAGTCTGTGGAAACAAATACGCATGCAAGATCAAGTGCATTAACTTGGAAAGCA 230  
 |||||

QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80  
 |||||  
 Db 231 CGACATGGATCTTGCACTATGCTTCCAGCTCAAGTGTATTGTCTACTTCCCTTGT 290  
 |||||

## RESULT 10

CD831479  
 LOCUS  
 DEFINITION  
 BN40.059J13F011208 BN40 Brassica napus cDNA clone BN40059J13, mRNA  
 sequence.  
 ACCESSION  
 CD831479  
 VERSION  
 CD831479.1 GI:32513419  
 KEYWORDS  
 EST.  
 SOURCE  
 Brassica napus (rape)  
 ORGANISM  
 Brassica napus  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
 1 (bases 1 to 438)  
 Genoplante.  
 Genoplante, a major partnership french program in plant genomics  
 Unpublished (2003)  
 Contact: Genoplante  
 Genoplante  
 93, rue Henri Rochefort 91025 EVRY CEDEX France  
 Tel: 33 1 69 47 54 00  
 Fax: 33 1 69 47 54 10  
 This sequence has been generated in the framework of the french  
 plant genomics programme 'Genoplante' (<http://www.genoplante.com>)  
 and <http://genoplante-info.infobiogen.fr/>.

## FEATURES

source  
 Location/Qualifiers  
 1. .438  
 /organism="Brassica napus"  
 /mol\_type="mRNA"  
 /cultivar="Jet Neuf"  
 /db\_xref="taxon:3708"  
 /clone="BN40059J13"  
 /tissue\_type="seed"  
 /clone\_lib="BN40"

## ORIGIN

Alignment Scores:  
 Pred. No.: 1,78e-41 Length: 438  
 Score: 436.00 Matches: 79  
 Percent Similarity: 98.8% Conservative: 0  
 Best Local Similarity: 98.8% Mismatches: 1  
 Query Match: 98.6% Indels: 0

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DB:                                     6          Gaps:          0
US-09-759-584-49 (1-80) x CD831479 (1-438)

QY 1 MetAlaLysPheAlaSerIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 20
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 51 ATGGCTAAGTTTGGCTTCCATCATTCGCCCTACTTTTGGCTGCTCTTGTCTCTTTCGCTGCT 110

QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 111 CTCGAAGCACCACCAATGTTGGAGCACAGAAAGTTGTGGAGAGGCCAAGTGGGACATGG 170

QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 171 TCAGAGTCTGTGGAAACAATAACGATCGAAGATCAGTGCATTAACTTGAAGAAGCA 230

QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 231 CGACATGGATCTTGCAACTATGTCTTCCAGCTCACAGTGTATTGTCTACTTCCCTTGT 290

RESULT 11
CD834008
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

CD834008 453 bp mRNA linear EST 10-JUL-2003
BN45.040E18F011019 BN45 Brassica napus cDNA clone BN45040E18, mRNA
sequence.
CD834008
CD834008.1 GI:32515948
EST.
Brassica napus (rape)
Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 453)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Genoplante.
Genoplante, a major partnership french program in plant genomics
Unpublished (2003)
Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).

FEATURES
source
1..453
/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jet Neuf"
/db_xref="taxon:3708"
/clone_lib="BN45040E18"
/tissue_type="seed"
/clone_lib="BN45"

ORIGIN
Alignment Scores:
Pred. No.: 1.86e-41 Length: 453
Score: 436.00 Matches: 79
Percent Similarity: 98.8% Conservative: 0
Best Local Similarity: 98.8% Mismatches: 1
Query Match: 98.6% Indels: 0
DB: 6 Gaps: 0

US-09-759-584-49 (1-80) x CD834008 (1-453)

QY 1 MetAlaLysPheAlaSerIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 20
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 51 ATGGCTAAGTTTGGCTTCCATCATTCGCCCTACTTTTGGCTGCTCTTGTCTCTTTCGCTGCT 110

QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 111 CTCGAAGCACCACCAATGTTGGAGCACAGAAAGTTGTGGAGAGGCCAAGTGGGACATGG 170

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QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 171 TCAGAGTCTGTGGAAACAATAACGATCGAAGATCAGTGCATTAACTTGAAGAAGCA 230

QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 231 CGACATGGATCTTGCAACTATGTCTTCCAGCTCACAGTGTATTGTCTACTTCCCTTGT 290

RESULT 12
CN726424
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

CN726424 453 bp mRNA linear EST 14-MAY-2005
3ETMS UP_003 H02_10JUN2003_001 Brassica napus 3ETMS Brassica napus
cDNA 5', mRNA sequence.
CN726424
CN726424.1 GI:65284226
EST.
Brassica napus (rape)
Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 453)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Tsang,B.
Gene expression in seed germination in Brassica napus
Unpublished (2004)
Contact: Ed Tsang
Plant Natural Products
National Research Council of Canada
Plant Biotechnology Institute, 110 Gymnasium Place, Saskatoon,
Saskatchewan, S7N 0W9, Canada
Tel: 306 975 4164
Fax: 306 975 4839
Email: Ed.Tsang@nrc-cnrc.gc.ca
High quality sequence stop: 453.
Location/Qualifiers
1..453
/organism="Brassica napus"
/mol_type="mRNA"
/db_xref="taxon:3708"
/clone_lib="Brassica napus 3ETMS"
/notes="Vector: pDNR-LIB_CREATOR; Site_1: SfiIA; Site_2:
SfiIB; Sequences have been trimmed to remove vector and
low quality regions using LUCY sequence cleanup software
(www.tigr.org)."

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## ORIGIN

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Alignment Scores:
Pred. No.: 1.86e-41 Length: 453
Score: 436.00 Matches: 79
Percent Similarity: 98.8% Conservative: 0
Best Local Similarity: 98.8% Mismatches: 1
Query Match: 98.6% Indels: 0
DB: 7 Gaps: 0

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US-09-759-584-49 (1-80) x CN726424 (1-453)

```

QY 1 MetAlaLysPheAlaSerIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 20
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 51 ATGGCTAAGTTTGGCTTCCATCATTCGCCCTACTTTTGGCTGCTCTTGTCTCTTTCGCTGCT 110

QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 111 CTCGAAGCACCACCAATGTTGGAGCACAGAAAGTTGTGGAGAGGCCAAGTGGGACATGG 170

QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 171 TCAGAGTCTGTGGAAACAATAACGATCGAAGATCAGTGCATTAACTTGAAGAAGCA 230

QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 231 CGACATGGATCTTGCAACTATGTCTTCCAGCTCACAGTGTATTGTCTACTTCCCTTGT 290

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RESULT 13
CN726661
LOCUS
DEFINITION
3ETMS UP 006_G02_10JUN2003_002 Brassica napus 3ETMS Brassica napus
cDNA 5', mRNA sequence.
ACCESSION
CN726661
VERSION
CN726661.1 GI:652844463
KEYWORDS
EST.
SOURCE
Brassica napus (rape)
ORGANISM
Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
1 (bases 1 to 456)
Tsang, E.
Gene expression in seed germination in Brassica napus
Unpublished (2004)
CONTACT
Ed Tsang
Plant Natural Products
National Research Council of Canada
Plant Biotechnology Institute, 110 Gymnasium Place, Saskatoon,
Saskatchewan, S7N 0W9, Canada
Tel: 306 975 4164
Fax: 306 975 4839
Email: Ed.Tsang@nrc-cnrc.gc.ca
High quality sequence stop: 456.
FEATURES
source
1..456
/organism="Brassica napus"
/mol_type="mRNA"
/db_xref="taxon:3708"
/clone_lib="Brassica napus 3ETMS"
/note="Vector: pDNR-LIB CREATOR; Site 1: SfiIA; Site 2:
SfiIB; Sequences have been trimmed to remove vector and
low quality regions using LUCY sequence cleanup software
(www.tigr.org)."
ORIGIN
Alignment Scores:
Pred. No.: 1..87e-41 Length: 456
Score: 436.00 Matches: 79
Percent Similarity: 98.8% Conservative: 0
Best Local Similarity: 98.8% Mismatches: 1
Query Match: 98.6% Indels: 0
DB: 7 Gaps: 0
US-09-759-584-49 (1-80) x CN726661 (1-456)
QY 1 MetAlaLysPheAlaSerIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaLa 20
Db 51 ATGGCTAAGTTTGTCTCCATCATTTGCTTCTTTTGTCTTCTTTTGTCTTCTTCT 110
QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTTP 40
Db 111 CTCGAAGCACCACCAATGTGTGAAGCAGCAAGATTGTGCGAGAGCCAAAGTGGACATGG 170
QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
Db 171 TCAGGAGTCTGTGGAACAACATACCGATCGCAAGATCATGATTAACCTTGAGAAAGCA 230
QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
Db 231 CGACATGGATCTTGCAACTATGCTTCCAGCTCACAAGTGATTGCTTCTTCTTCTTCT 290
RESULT 14
CD828332
LOCUS
DEFINITION
BN25_070H07F020125 BN25 Brassica napus cDNA clone BN25070H07, mRNA
sequence.
ACCESSION
CD828332
VERSION
CD828332.1 GI:32510272
KEYWORDS
EST.
SOURCE
Brassica napus (rape)
ORGANISM
Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
1 (bases 1 to 553)
Genoplante, a major partnership french program in plant genomics
Unpublished (2003)
CONTACT
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).
FEATURES
source
1..480
/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jet Neuf"
/db_xref="taxon:3708"
/clone="BN25070H07"
/tissue_type="seed"
/clone_lib="BN25"
ORIGIN
Alignment Scores:
Pred. No.: 2e-41 Length: 480
Score: 436.00 Matches: 79
Percent Similarity: 98.8% Conservative: 0
Best Local Similarity: 98.8% Mismatches: 1
Query Match: 98.6% Indels: 0
DB: 6 Gaps: 0
US-09-759-584-49 (1-80) x CD828332 (1-480)
QY 1 MetAlaLysPheAlaSerIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaLa 20
Db 41 ATGGCTAAGTTTGTCTCCATCATTTGCTTCTTTTGTCTTCTTTTGTCTTCTTCT 100
QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTTP 40
Db 101 CTCGAAGCACCACCAATGTGTGAAGCAGCAAGATTGTGCGAGAGCCAAAGTGGACATGG 160
QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
Db 161 TCAGGAGTCTGTGGAACAACATACCGATCGCAAGATCATGATTAACCTTGAGAAAGCA 220
QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
Db 221 CGACATGGATCTTGCAACTATGCTTCCAGCTCACAAGTGATTGCTTCTTCTTCTTCT 280
RESULT 15
CD831014
LOCUS
DEFINITION
BN40_047K12F011228 BN40 Brassica napus cDNA clone BN40047K12, mRNA
sequence.
ACCESSION
CD831014
VERSION
CD831014.1 GI:32512954
KEYWORDS
EST.
SOURCE
Brassica napus (rape)
ORGANISM
Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
1 (bases 1 to 553)
Genoplante, a major partnership french program in plant genomics
Unpublished (2003)
CONTACT
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France

```

Tel: 33 1 69 47 54 00  
Fax: 33 1 69 47 54 10  
This sequence has been generated in the framework of the french  
plant genomics programme 'Genoplante' (<http://www.genoplante.com>)  
and <http://genoplante-info.infobiogen.fr>.

FEATURES

source  
1..553  
/organism="Brassica napus"  
/mol\_type="mRNA"  
/cultivar="Jet Neuf"  
/db\_xref="taxon:3708"  
/clone="BN40047K12"  
/tissue\_type="seed"  
/clone\_lib="BN40"

ORIGIN

Alignment Scores:  
Pred. No.: 2.4e-41 Length: 553  
Score: 436.00 Matches: 79  
Percent Similarity: 98.8% Conservative: 0  
Best Local Similarity: 98.8% Mismatches: 1  
Query Match: 98.6% Indels: 0  
DB: 6 Gaps: 0

US-09-759-584-49 (1-80) x CD831014 (1-553)

QY 1 MetAlaLysPheAlaSerIleIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 20  
|||  
Db 50 ATGGCTAAGTTGCTTTCCATCATTTGCCCTACTTTTGTGCTGCTCTTTGCTGCTGCT 109  
|||  
QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40  
|||  
Db 110 CTCGAGACCAACAATGGTGGAGCACAGAGTTGTGGAGAGGCCAAGTGGACATGG 169  
|||  
QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60  
|||  
Db 170 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGATCAGTGCATTAACTTGAGAAAGCA 229  
|||  
QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80  
|||  
Db 230 CGACATGGATCTTGCAACTATGTCTTCCAGCTCACAGGTGATTGTTGCTACTTCCCTTGT 289  
|||

Search completed: May 10, 2006, 09:42:57  
Job time : 3004.5 secs